

# **FIGURE 1**

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCCACCGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTCGCTTCCCG  
CAGCGCTACCCGCCATGCGCCTGCCGCCGGCGCTGGGCTCCTGCCGCTTCTGCTG  
CTGCTGCCGCCGCCGGAGGCCAAGAAAGCCGACGCCCTGCCACCAGGTGCCGGGGCT  
GGTGGACAAGTTAACCAAGGGATGGTGACACCGCAAAGAAGAACTTGGCGGGAAACA  
CGGCTTGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC  
CTGGAGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA  
GCACCTGGAGGCCTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGTGTCTCGCATGC  
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGGCCACTGCAGCGGAGATGGAGCAGACA  
GGCGACGGGTCCGCCGGTGCACATGGGTACCAGGGCCGCTGTGACTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCAGCGAGTGTGAAGTGGCTGGTGCT  
GGACGAGGGCGCCTGTGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTG  
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG  
GGCTGCACAGGGAAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA  
CGGACAGTGTGCAAGATGTGGACGAGTGTCACTAGCAGAAAAAAACCTGTGAGGAAAAACG  
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGCTGACGGCTTCGAAGAAACG  
GAAGATGCCTGTGCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT  
GCCCTCCCGCAAGACCTGTAATTGTGCCGGACTTACCCCTTAAATTATTGAGAAGGATGTCC  
CGTGGAAAATGTGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGGGGAGAGGCTGC  
CTGCTCTCAACGGTTGATTCTCATTGTCCTTAAACAGCTGCATTCTGGTTGTTCTTA  
AACAGACTTGTATATTTGATACAGTTCTTGTAATAAAATTGACCATTGTAGGTAATCAGG  
AGGAAAAAAAGGGCGCCGCGACTCTAGAGTCGACCTGCAGAAGC  
TTGGCCGCCATGGCCAACCTGTTATTGAGCTTATAATGGTTACAAATAAGCAATAGCA  
TCACAAATTCAAAAGCATTTCAGTGCATTCTAGTTGTGGTTGTCACAAACTC  
ATCAATGTATCTTATCATGTCGGATCGGAATTAAATTGGCGCAGCACCATGGCCTGAAAT  
AACCTCTGAAAGAGGAACCTGGTAGGTACCTCTGAGGGCGAAAGAACCAAGCTGTGGAATG  
TGTGTCAGTTAGGGTGTGAAAGTCCCCAGGCTCCAGCAGGCAGAAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTT

## FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLPLLLLPPAPEAAKKPTPCHRGRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL  
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG  
NGHCSDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNEHTSIC\_TACDESCKTCGTLNRDCGECEVGVLDE  
GACVDVDECAAEP PCSAAQFCKNANGSYTCECDSSCVGCTGEGPGNC E C I S G Y A R E H G Q C A D V D E C S L A E K T  
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

**Signal peptide:**

amino acids 1-24

**N-glycosylation sites.**

amino acids 190-194 and 251-255

**Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

**Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

**Tyrosine kinase phosphorylation site.**

amino acids 303-310

**N-myristoylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

**Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

**EGF-like domain cysteine pattern signature.**

amino acids 166-178

**Leucine zipper pattern.**

amino acids 94-116

## **FIGURE 3**

CAGGTCCAAC TGCACCTCGTTCTATGATTGAATTCCCCGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACGCGTCCGCCAGGCCGGAGGCAGCGCAGCGCAGAGTATCTGACGGGCCAGCGTCTAAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGGCCAGGGTAGGTGCGTAGGTGCG  
GCACGAGGAGTTTCCCGCAGCGAGGAGGAGCCTGTACCTATGGATCGATGCTCACCAAGGAAAGAGTACTCA  
CTGGCCGCCGCTCTGGCTCTGGAGCATCCTCTGTGCCTGCTGGACTGCGGCCGGAGGC  
CGGGCCGCCGAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAAGGAAAGAGTACTCA  
TAGGATTGAAGAAGATATCCTGATTGTTAGAGGGAAAATGGCACCTTTACACATGAT  
TTCAGAAAAGCGAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTCAC  
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGTCTTGCGCTCCCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGAAACAGTGCTCACAAAGGCA  
TCAGTTGTTCAAGTTGGTTCCATGTCTTGAAAACAGGATGGGTGGCAGCATTGAAGT  
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAAATGCTATCT  
TCTTTAAACATGTCAACAAAGCTGAGTGCCCAGGCAGGTGGCAAATGGAGGCTTTGTAAT  
GAAAGACGCATCTGCAGTGTCCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG  
TACCCACGATGTATGAATGGTGGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG  
GATTCTATGGAGTGAACTGTGACAAAGCAAACCTGCTCAACCACCTGCTTAAATGGAGGGACC  
TGTTCTACCCCTGGAAAATGTATTGCCCTCAGGACTAGAGGGAGAGCAGTGTGAAATCAG  
CAAATGCCACAACCTGCGAAATGGAGGTAAATGCATTGGTAAAGCAAATGTAAGTGT  
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGCTGCGAGCCTGGCTGTGGTCACAT  
GGAACCTGCCATGAACCCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGCAGC  
ACACGCCCTCACTAAAAAGGCCAGGGAGCGGGATCCACCTGAATCCAATTACATCTGG  
**TGA**ACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTCATAGCCTTGTAAACCTTCA  
TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGGCCTGAATTATTAGCT  
TCATTATAAAACTACTGAGCTGATATTACTCTCCTTTAAGTTCTAAGTACGTCTGTAG  
CATGATGGTATAGATTCTTGTGCTTCAAGTGTAGTTGGCAGATATTCAAAATTACAATGCATTATGGT  
TCAGGTTAAAATTTCAGTGTAGTTGGCAGATATTCAAAATTACAATGCATTATGGT  
GTCTGGGGCAGGGAAACATCAGAAAGGTTAAATTGGGAAAAATGCGTAAGTCACAAGAAT  
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTCAAGATTATTGTCAAGATATTAGAT  
GTTGTTACATTAAAAATTGCTCTAATTAAACTCTCAATAACAAATATTGGAC  
TTACCAATTCCAGAGATTCACTGATTAAAAAAATTACACTGTGGTAGTGGCATTT  
AAACAAATATAATATTCTAAACACAAATGAAATAGGGAAATAATGTATGAACCTTTGCAT  
TGGCTTGAAGCAATATAATATTGAAACAAAACACAGCTCTACCTAATAACATTTTAT  
ACTGTTGTATGTATAAAATAAAGGTGCTGCTTAGTTTTGGAAAAA  
AAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC  
CGCCATGGCCAAC TTGTTATTGCAGCTTATAATG

## FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094  
><subunit 1 of 1, 379 aa, 0 stop  
><MW: 41528, pI: 7.97, NX(S/T): 2  
MARRSAFPAAALWLWSILLCLLRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK  
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPPLL  
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC  
RNGGFCNERRICECPDGFHGPCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST  
TCFNGGTCFYPGKICPPGLEGEQCEISKCPQPCRNGGKIGKSCKCSKGYQGDLCSPV  
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP  
PESNYIW

**Signal peptide:**

amino acids 1-28

**N-glycosylation site.**

amino acids 88-92, 245-249

**Casein kinase II phosphorylation site.**

amino acids 319-323

**Tyrosine kinase phosphorylation site.**

amino acids 370-378

**N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

**EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## **FIGURE 5**

CGGACGCGTGGCGTCCGGCGTCGCAGAGCAGGAGGCCAGGAGGCCAGCCTGGG  
CCCCAGCCCACACCTCACCAAGGGCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTAC  
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGCTCGGGCAGCAGGGCTGAGGCCGG  
GAGCTAGCACCGGGTCTGCACCTGCAGGGCATCCGGACGCGGGAGGCCGGTACTGCCAGGA  
GCAGGACCTGTGCTGCCGCGGCCGTGCCAGCAGACTGTGCCCTGCCACTCGGGCAGGCCATCT  
GTTACTGTGACCTCTCTGCAACCGCACGGCTCCGACTGCTGCCCTGACTTCTGGGACTTC  
TGCCTCGGCGTGCCACCCCTTTCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA  
TCCAGTCTTGGAACGTACTGGACAACGTAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT  
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG  
GAACCACAGCGCCTCTGGGGCATGACCCTGAGGGCATTGCTACCGCCTGGCACCA  
TCCGCCATCTCCTCGGTATGAACATGCATGAAATTATAACAGTGTGAACCCAGGGGAG  
GTGCTTCCCACAGCCTCGAGGCCTCTGAGAAAGTGGCCAACCTGATTGATGAGCCTTTGA  
CCAAGGCAACTGTGCAGGCTCTGGGCCTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT  
CAATCCATTCTCTGGGACACATGACGCCGTCTGTGCCAGAACCTGCTGTCTTGAC  
ACCCACCAGCAGCAGGGCTGCCGCGTGGCGTCTCGATGGTGCCTGGTGGTCTGCGTCG  
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAAACGAGACGAGGCTGGCC  
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCC  
CACTGCCAACAGCTATGTTAATAACAATGACATCTACAGGTCACTCCTGTCTACCGCCT  
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAAATGGCCCTGTCCAAGCCCTCA  
TGGAGGTGCATGAGGACTTCTCCTATAACAAGGGAGGCATCTACAGCCACAGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATACGCCGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG  
AGAGGAGACGCTGCCAGATGGAAGGACGCTAAATACTGGACTGCCAACTCCTGGGCC  
CAGCCTGGGGCGAGAGGGCCACTTCCGCATCGTGCAGGCCGTCAATGAGTGCACATCGAG  
AGCTTCGTGCTGGCGCTGGGCGCGTGGGATCCAGGCTAACGGCCGGGAGAGGCCCAATG  
GGCGGTGACCCAGCCTGCCGACAGAGCCGGCGCAGGCCGGCAGGGCGCTAACGGCC  
CCCAGCGCGGTTCCGCTGACGCAGGCCCGCTGGGAGGCCGGCAGGCAGACTGGCG  
GAGCCCCAGACCTCCAGTGGGACGGGCAGGGCTGGCTGGGAAGAGCACAGCTGCAG  
ATCCCAGGCCCTGGCGCCCCACTCAAGACTACCAAGCCAGGACACCTCAAGTCTCCAGC  
CCCAATACCCACCCCAATCCGTATTCTTTTTTTTTAGACAGGGTCTTGCTCCG  
TTGCCCAAGGTTGGAGTGCAGTGGCCATCAGGGCTACTGTAACCTCCGACTCCTGGTTCA  
AGTACCCCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCACACCTGGC  
TAATTTTGATTTTGTAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAACCT  
CCTGGGCTCAAGCGGTCCACCTGCCCTCCAAAGTGTGGATTGCAGGCATGAGGCC  
ACTGCACCCAGCCCTGTATTCTTATTTCAGATATTATTTCTTCACTGTTAAAAA  
TAAAACCAAAGTATTGATAAAAAAAAAAA

## **FIGURE 6**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223  
><subunit 1 of 1, 164 aa, 1 stop  
><MW: 18359, pI: 7.45, NX(S/T): 1  
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAAGGRYCQEQLCCRGRADDC  
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPIQGCMHGGRIYPVLGYWDNCNR  
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG
```

**N-glycosylation site.**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

**N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

**Amidation site.**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

## **FIGURE 7**

AGGCTCCTGGCCCTTTCCACAGCAAGCTNTGCNATCCGATTGTTGTCTCAAATCCA  
ATTCTCTTGGGACACATNACGCCGTCTTCCTTNGCCCCAGAACCTGCTGTCTTGACACCCAC  
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTTCCCTGCGTCGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGGCAAGGCCAGGCCACTGCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACGCCCTGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTATGGAGG  
TGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTTGGG  
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

## **FIGURE 8**

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCAGTGCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG  
GAGCAGTGCTGGACC CGCGCATCCCGCGAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG  
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCTGCAGCCGGCTGCCGCCATCCTT  
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGACCCGGCCAGCTATAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCCAGTGGGAGCCTGTCCCTGGTTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCCACCCCTGACCCCTCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA  
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCCTCTGCTGCTGTTTC  
CATGGCCCAGCATTCTCCACCCCTTAACCCCTGTGCTCAGGCACCTCTCCCCCAGGAAGCCTT  
CCCTGCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA  
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA  
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA  
GGGGCCAGGCCTCACATTGTTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
AATAAACACCTGTTGGATAAGCCAAAAAAA

## **FIGURE 9**

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSLSDT  
DPPADGPSNPLCCCFFGPAFSTLNPLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

**Signal peptide:**

amino acids 1-47

**N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

**Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

**N-myristoylation site.**

amino acids 56-60

**Amidation site.**

amino acids 70-74

## **FIGURE 10**

CCACCGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCGCTGCTGCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGGCCATGACC  
GACCAGCTGAGCAGGGGGCAGATCCCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTCAGGTCAACGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC  
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGAAGAGCAAAGACTG  
CGTGGTCACGGAGATCGTGTGGAGAACAACTATAACGCCCTCCAGAACGCCGGCACGAGG  
GCTGGTTCATGGCCTTCACCGGCAGGGCGGCCAGGCTTCCGCAGCCGCCAGAAC  
CAGCGCGAGGCCCACTTCATCAAGCGCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC  
CGAGAACAGAAGCAGTCGAGTTGTGGCTCCGCCACCCGCCGACCAAGCGCACAC  
GGCGGCCCAGCCCCCTACGTAGTCTGGAGGCAGGGGCAGCAGCCCCCTGGCCGCCTCCC  
CACCCCTTCCCTTAAATCCAAGGACTGGCTGGGTGGCAGGGGAGCCAGATCCCC  
GAGGGAGGACCCCTGAGGGCCCGAAGCATCCGAGCCCCAGCTGGGAAGGGCAGGCCGGTG  
CCCCAGGGCGGCTGGCACAGTGCCCTCCGGACGGTGGCAGGCCCTGGAGAGGAAC  
GAGTGTACCCGTATCTCAGGCCACCAGCCTGCGCCGCCCTCCAGCCGGCTCCTGAAGCC  
CGCTGAAAGGTCACGACTGAAGGCCTTGCAGACAACCGTCTGGAGGTGGCTGTCCCTAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCCAGCCCCAAACTCCTCCGGTAGACTGTA  
GGAAGGGACTTTGTTGTTGTTGTTCAGGAAAAAAAGAAAGGGAGAGAGAGGAAAATAG  
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCACTCCAGCCC  
CGGAATAAAACCATTTCTGC

## FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI  
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGSKDCVFTEIVLE  
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQQQFEF  
VGSAPTRRTKRTRRPQPLT

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128

## **FIGURE 12**

ACTTGCCATCACCTGTTGCCAGTGTGGAAAATTCTCCCTGTTGAATTTCACATGGAG  
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT  
CATTGGATTTGCTGTTATTTTTCTTTCTTTCCCACCAATTGTATTTAT  
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGCTTTCT  
GAAGTCTGGCTTATCATTCCCTGGGGCTCTACTCACAGGTGTCACACTCCCTGGCCTGCC  
CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTGACCTCAGTG  
CCTCTGGGATCCCAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAAATAATGC  
TGGATTCCTGCAGAACTGCACAATGTACAGTCGGTGACACGGCTACCTGTATGGCAACC  
AACTGGACGAATTCCCCATGAACCTTCCAAGAAATGTCAGAGTTCTCCATTGCAGGAAAC  
AATATTCAAGACCAATTTCACGGCTGCTTGCCCCAGCTTGAAGCTTGAAGAGCTGCACCT  
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCTTCCGGAGGCTATTAGCC  
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGCTTCCGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCCGACATGGCCTCCAGAA  
TCTCACGAGCTTGGAGCGTCTTATTGTTGACGGAACCTCCTGACCAACAAAGGTATGCCG  
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTAATTGCTGTCC  
CACCCCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACCAAGAT  
AAACACATTCCCTTGACAGCCTCTCAAATCTCGTAAGCTGGAACGGCTGGATATATCCA  
ACAACCAACTGCGGATGCTGACTCAAGGGTTTTGATAATCTCCAACCTGAAGCAGCTC  
ACTGCTCGGAATAACCCCTGGTTTGACTGCAGTATTAAATGGGTACAGAATGGCTCAA  
ATATATCCCTTCATCTCAACGTGCGGGTTCATGTGCCAAGGTCTGAACAAGTCCGGG  
GGATGGCCGTCAAGGAATTAAATATGAATCTTGTCCCTGCCCACCGACCCCCGGCCTG  
CCTCTCTCACCCAGCCCCAAGTACAGCTTCTCGACCAACTCAGCCTCCACCCCTCTAT  
TCCAAACCTAGCAGAAGCTACAGCCTCCAACCTCCTACACATCGAAACTTCCCACGATT  
CTGACTGGGATGGCAGAGAAAGAGTGAACCCACCTATTCTGAACGGATCCAGCTCTATC  
CATTGTTGAATGATACTTCAAGTCAGCTGGCTCTCTCTTCAACCGTGATGGCATA  
CAAACTCACATGGGTAAAATGGCCACAGTTAGTAGGGGGCATCGTCAGGAGCGCATAG  
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT  
TGTTAGTGCCACTGGATGCTTTAACTACCGCGCGTAGAAGACACCATTGTTCAGAGGC  
CACCAACCATGCCTCTATCTGAACAAACGGCAGCAACACAGCGTCCAGGCATGAGCAGACGA  
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGATGGGGGGCGGTGATATT  
GTGCTGGTGGTCTTGCTCAGCGTCTTGTGCTGGCATATGCACAAAAGGGCGCTACACCTC  
CCAGAAGTGGAAATACAACCGGGCCGGCGAAAGATGATTATTGCGAGGCAGGCACCAAGA  
AGGACAACCTCCATCCTGGAGATGACAGAAACCAAGTTTCAAGATCGTCTCTAAATAACGAT  
CAACTCCTAAAGGAGATTCAGACTGCAGCCATTACACCCCCAAATGGGGCATTAATTA  
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC  
ACTGCCATACTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA  
CACACTCGTGTGTCACATAAAGACACGCAGATTACATTGATAAAATGTTACACAGATGCAT  
TTGTCATTTGAATACTCTGTAATTACGGTGTACTATATAATGGGATTAAAAAGTG  
CTATCTTCTATTCAAGTTAATTACAAACAGTTGTAACCTTGTCTTTAAATCTT

## **FIGURE 13**

MGLQTTKWPShGAFFLKSLLIISLGLYSQVSLLACPSVCRCDRNFVYCNERSLTSVPLGIP  
EGVTVLYLHNNQINNAGFPaelHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI  
SRAALAQLLKLEELHLDNSISTVGVEDGAFREAIISLKLFLSKNHLSVPVGLPVDLQELR  
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKEFSIVRNSLSHPPPD  
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARN  
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMARVELNMNLLSCPTTPGLPLFTP  
APSTASPTTQPPTLSIPNPSRSYTPPTSKLPTIPDWDGRERVTTPPISERIQLSIHFVND  
TSIQVSWLSSLFTVMAYKLTWVKGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL  
DAFNYRAVEDTICSEATTHASYLNNGNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLUVL  
LSVFCWHMHKKGRYTSQWKYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNNDQLLKG  
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

## FIGURE 14

ACTTGGAGCAAGCGCGGCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGCTCCGTCCGCCTCCCACGAGCG  
ATCCCCGAGGAGAGCCGCGGCCCTCGCGAGGCAGAGGCCAGGAGAACCCGGGTGGCTCGCCCCCTGCC  
TCGCTTCCCAGGCCGGCGCTGCAGCCTTGCCCCCTCTGCTCGCCTTGAAAATGGAAAAGATGCTCGCAGGCT  
GCTTCTGCTGATCCTCGACAGATCGCCTCCCTGCCAGGGCAGGGAGCGGTACAGTGGGAGGTCCATCT  
CTAGGGCAGACAGCTCGGACCCACCCGCAGACGCCCTCTGGAGAGTCTGTGAGAACACAAGGGCAGACC  
TGGTTTCATCATTGACAGCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGGAGTTCATCGTGGACA  
TCTTGCAATTCTGGACATTGGTCTGTGACAGTCCAGGAGTGGCCCTGCTCCAATATGGCAGCACTGTCAAGAATG  
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCAGGGTGGAGCTGCTCAAGAGGATGCGGCATCTGTCCACGG  
GCACCATGACTGGCTGGCATCCAGTATGCCCTGAAACATCGCATTCTCAGAACAGCAGAGGGGGCCGGCCCTGA  
GGGAGAATGTGCCACGGGTATAATGATCGTACAGATGGGAGACCTCAGGACTCCGTGGCCAGGGTGGCTGCTA  
AGGCACGGGACACGGGCATCTTAATCTTGCCATTGGTGTGGCCAGGTAGACTTCACACCTTGAAGTCCATTG  
GGAGTGAGCCCCATGAGGACCATGTCTTCTTGTGGCAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTCC  
AGAAGAAGTTGTGCA CGGGCACATGTGCAGCACCCCTGGAGCATAACTGTGCCACTCTGCATCAACATCCCTG  
GCTCATACTGCTGCAGGTGCAAACAAGGCTACATTCTCACTCGGATCAGACGACTTGCAGAATCCAGGATCTGT  
GTGCCATGGAGGACCACAACGTGAGCAGCTGTGTGAATGTGCGGGCTCTCGTCTGCCAGTGCTACAGTG  
GCTACGCCCTGGTGGAGGATGGGAAGAGGTGTGTGGCTGTGACTACTGTGCCCTAGAAAACCACGGATGTGAAC  
ATGAGTGTGAAATGCTGATGGCTCTACCTTGCCAGTGCATGAAGGATTGCTCTTAACCCAGATGAAAAAA  
CGTGACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT  
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGAAAACCTGCAGCCAGTGACACTGTGCCAC  
AGCAGGACCATGGCTGTGAGCAGCTGTGTGAACACCGAGGATTCTTCTCGTCTGCCAGTGCTCAGAAGGCTCC  
TCATCAACGAGGACCTCAAGACCTGCTCCGGGTGGATTACTGCCCTGCTGAGTGACCATGGTTGTGAATACTCCT  
GTGTCACATGGACAGATCTTGCTGTCAGTGTCTGAGGGACACGTGCTCCGCAGCGATGGGAAGACGTGTG  
CAAAATTGGACTCTTGCTCTGGGGACCACGGTTGTGAACATTGTGTGAAGCAGTGAAGATTGTTGTGT  
GCCAGTGCTTGAAGGTATATACTCCGTGAAGATGGAAAACCTGCAGAAGGAAGAGTGTCTGCCAAGCTATAG  
ACCATGGCTGTGAACACATTGTGAACAGTGCAGACTCATACACGTGCGAGTGCTTGGAGGGATTCCGGCTCG  
CTGAGGATGGGAACCGCTGCCGAAGGAAGGATGTCTGCAAATCAACCCACCATGGCTGCGAACACATTGTGTTA  
ATAATTGGAAATTCTCATCTGCAAATGCTCAGAGGGATTGTTCTAGCTGAGGACGGAAGACGGTCAAGAAAT  
GCACTGAAGGCCAATTGACCTGGCTTGTGATCGATGGATCCAAGAGTCTGGAGAAGAGAATTGAGGTCG  
TGAAGCAGTTGTCACTGAAATTATAGATTCTTGACAAATTCCCCAAAGCCGCTCGAGTGGGCTGCTCCAGT  
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACCTCAACTCAGCAAAGACATGAAAAAAGCCGTGGCCC  
ACATGAAATACATGGGAAGGGCTTATGACTGGCTGCCCTGAAACACATGTTGAGAGAAGTTTACCCAAG  
GAGAAGGGCCAGGCCCTTCCACAAGGGTGCCAGAGCAGCATTGTGTTACCGAGGACGGGCTCAGGATG  
ACGTCCTGGAGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTTGGGTAGGAAAGCCATTG  
AGGAGGAACATACAAGAGATTGCCCTGAGCCCACAAACAAGCATCTTCTATGCCGAAGACTTCAGCACAATGG  
ATGAGATAAGTAAAAACTCAAGAAAGGCATCTGTGAAGCTTAGAAGACTCCGATGGAAGACAGGACTCTCCAG  
CAGGGAACTGCCAAAACGGTCCAACAGCCAACAGAACATCTGAGCCAGTCACCATATAATCCAAGACCTACTTT  
CCTGTTCTAATTGCACTGCAACACAGATATCTGTTGAAGAAGACAATCTTACGGTCTACACAAAGCTTT  
CCCATTCAACAAACCTCAGGAAGCCCTTGGAAAGAAAACACGATCAATGCAAATGTGAAAACCTTATAATGT  
TCCAGAACCTGCAAACGAAGAAGTAAGAAAATTAAACACAGCGCTTAGAAGAAATGACACAGAGAACGGCC  
TGGAAAATGCCCTGAGATAACAGATGAAGATTAGAAATCGCAGACACATTGAGTCATTGTATCACGGATTACAAT  
GAACCGAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGAGTAAACAAATCAGTACTGA  
GAAACCTGGTTGCCACAGAACAAAGACAAGAAGTATACTAACTTGTATAAATTATCTAGGAAAAAAATCCT  
TCAGAATTCTAAGATGAATTACCAAGGTGAGAATGAATAAGCTATGCAAGGTATTGTAATATACTGTGGACAC  
AACTGCTCTGCCCTCATCTGCCCTAGTGTGCAATCTCATTGACTATACGATAAAAGTTGCACAGTCTTACTT  
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTGTACTGGACTTACCTTGATATATGTATATGGATGTATG  
CATAAAATCATAGGACATATGTACTTGTGGAACAAGTGGATTTTTATAACATATAAAATTCAACACTTCAG

## **FIGURE 15**

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGRHARTHPOQTALLESSCENKRADLVFII  
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFRKSEVERAV  
KMRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD  
TGILIFAIQVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN  
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNPVGSFVCQCYSGYA  
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKGPC  
EHECVNMEESYYCRCHRGYTLDPNGKTCSRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI  
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSRGKTCAKLDSCALGDHGCE  
HSCVSSEDSFVCQCFCFGYILREDGKTCCRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRRA  
EDGKRCRRKDVKSTHHGCEHICVNNNGNSYICKCSEGFWLAEDGRRCKCTEGPIDLVFVID  
GSKSLGEENFEVVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA  
HMKYMGKGSMTGLALKHMERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN  
GITMYAVGVGKAIEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEALEDSDGRQDS  
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL  
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

**Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
781-785, 819-823, 866-870

**N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
639-645, 690-696, 752-758, 792-798

**Amidation site.**

amino acids 314-318, 560-564, 601-605

**Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## **FIGURE 16**

GGAGCCGCCCTGGGTGTCAGCGGCTGGCTCCCGCGCACGCTCCGGCGTCGCAGCCTCG  
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCCGCCAGGGAGGGC  
**CATG**ATTCCCTCCGGGCCCCCTGGTACCAACTTGCTGCCGTTTGTCTGGGCTGA  
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACCTGCCGCCAACCGGTTGCAG  
GCGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACCTGCACGGGAGGTGTCTTC  
ATCCCAGCCATGGGAGGTGCCCTTGATGTGGTTCTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC  
ATGCCCTCCCGAACCTGTCCCTGCCGCTGGAGGGCTCCAGGAGAAAGACTCTGGCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGCAAATCTAGGGCCACAGCATAAAACCT  
TAGAACTCAATGTACTGGTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT  
GTGGGGCAAACGTGACCCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGACCAGCATTAGATGTCATCCGTG  
GGTCTTAAGCCTACCAACCTTCGTCTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGC  
AGTGGTTGGAGCTGTTGGGTACCCCTGGTTGGACTGGGGTGTGGCTGGCTGGTCC  
TCTTGTACCAACGCCGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC  
ATTGCTCCCCGGACCCCTGCCCTGGCCAAGAGCTCAGACACAATCTCAAGAATGGGACCC  
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCATGCCCTCCAGGCCTGGTGCAT  
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT  
GGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG  
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTAT**GATGAC**  
CCCACCACTATTGGCTAAAGGATTGGGTCTCTCCTATAAGGGTCACCTCTAGCAC  
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCAACCTCTC  
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTGAGTCTCCAGGC  
CCCCCTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTCAAGCTGGCTGGTTAGGTTTACTGGGCAGAGGATAGGAAATCTC  
TTATTAAAACATGAAATATGTGTTTTCAATTGCAAATTAAATAAGATAACATAA  
TGTTGTATGAAAAA

## FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKDSGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKP  
AVQYQ WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGT  
AQCNVTLEVSTGPGAA VVAGAVVGT  
LVGLGLLAGLVLLYHRRGKALEEPANDIKA  
DAIA  
PRTLPWP  
KSSDTISKNGTL SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHP  
QP  
ISPIPGGVSSSGLSR MGAVPVMVPAQS  
QAGSLV

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267

**N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

**N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

## **FIGURE 18**

CGCCACCACTGCGGCCACGCCA**ATGAAACGCCTCCGCTCCTAGGGTTTCCACTTG**  
TTGAATTGTCCTATACTCAAAATTGCACCAAGACACCTGTCTCCAAATGAAAATGTGA  
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA  
TTTGTGAAGATGATAATGAATGTGAAATTAACTCAGTCCTGTGGAAAATGCTAATTGC  
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTCAGATCCAGCAGTAACCA  
AGACAGGTTATCAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGCCATT  
TAGATAATGTCTGTATAGCTGCAAATTAAATAAAAACCTTAACAAAAATCAGATCCATAAAA  
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA  
TATAATTACATATAGAAATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAAACA  
CTATCTCAGCCAAGGACACCCCTTCTAACTCAACTCTTACTGAATTGAAAAACCGTGAAT  
AATTTGTTCAAAGGGATACATTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC  
ACATCTTACAAAACACTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC  
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTGAT  
TCATATAACATGAAACATATTCACTCCTCATATGAATATGGATGGAGACTACATAAATATA  
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGAGTTGCATTTCATTTATATA  
AGAGTATTGGCTTGTCTTCATCATCTGACAACCTTCTTATTGAAACCTCAAATTATGAT  
AATTCTGAAGAGGGAGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCC  
ACCCACATTATATGAACCTGAAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATA  
GGTATAGGAGTCTATGTGATTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT  
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT  
GACACATTGCAATTGATGTCCTCTGGCCTTCATTGGTATTAAAGATTATAATATTC  
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGCTTGCCATATGCATTTT  
ACCTCTGGTCTTCAGTGAATTCAAAGCACCAGGACAACAATTCAACAAAATCTTGCTG  
TAGCCTATTCTTGCTGAATTGTTCTTGTGGATCAATACAAATACTAATAAGCTCT  
TCTGTTCAATCATTGCCGACTGCTACACTACTCTTTAGCTGCTTGCATGGATGTGC  
ATTGAAGGCATACATCTCATGTTGTGGTGTCACTACAACAAAGGGATTGGCA  
CAAGAATTTTATATCTTGCTATCTAACGCCAGCCGTGGTAGTTGGATTTCGGCAGCAC  
TAGGATACAGATATTATGGACAACAAAGTATGTTGGCTTAGCACCGAAAACAACCTTATT  
TGGAGTTTATAGGACCAAGCATGCCTAATCATTCTGTTAATCTCTGGCTTGGAGTCAT  
CATATACAAAGTTTCGTACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTGAGAAC  
TAAGGTCTTGTGCAAGAGGGAGCCCTCGCTCTCTGTTCTCGGCACCACCTGGATCTT  
GGGGTTCTCCATGTTGTGCACGCATCAGGGTACAGCTTACCTCTCACAGTCAGCAATGC  
TTTCAGGGGATGTTCATTTTATTCTGTGTTTATCTAGAAAGATTCAAGAAGAAT  
ATTACAGATTGTTCAAAATGCCCCGTGTTGGATGTTAAGG**TAAACATAGAGAATG**  
**GTGGATAATTACAACGTGACAAAATAAAATTCCAAGCTGTGGATGACCAATGTATAAAA**  
**TGACTCATCAAATTATCCAATTATTAACACTAGACAAAAGTATTAAATCAGTTTCT**  
**GTTTATGCTATAGGAACGTGAGATAATAAGGAAAATTATGTATCATATAGATATACTATGT**  
**TTTCTATGTGAAATAGTTCTGTCAAAATAGTATTGCAAGATATTGAAAGTAATTGGTT**  
**CTCAGGAGTGTATCACTGCACCCAGGAAAGATTCTTCTAACACAGAGAAGTATATGAA**  
**TGCTGTAAGGAAACCACTGGCTGATATTCTGTGACTCGTGTGCTTGAACACTAGTCC**  
**CCTACCCACCTCGGTATGAGCTCATTACAGAAAGTGGAACATAAGAGAATGAAGGGCAGA**  
**ATATCAAACAGTGAAAAGGAATGATAAGATGTATTGAAATGAACTGTTTCTGTAGAC**  
**TAGCTGAGAAATTGTTGACATAAAAGAATTGAAGAAACACATTTCACCATTGAA**  
**TTGTTCTGAACCTAAATGTCCACTAAAACAACCTAGACTCTGTTGCTAAATCTGTTCTT**  
**TTCTAATATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA**  
**AAAAAAAAAAAAAAAAAAAAAA**

## FIGURE 19

MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC  
GNLTQSCGENANCTNTEGSYYCMCVPGRSSSNQDRFITNDGTVCIENVANCHLDNV CIAA  
NINKTLTKIRSIKEPVALLQEYVRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL  
SNSTLTFVKTVNNFVQRDTFVVWDKLSVNHRRTLTKLMHTVEQATLRIQSFFQKTTEFDT  
NSTDIALKVFFFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS  
SSDNFLLPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF  
WNYSPDTMNGWSSEGCELYSNETHSCRCNLTHFAILMSSGPSIGIKDYNILTRITQLG  
IIISLICLAI CIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFC SIIAGL  
LHYFFLAFAFWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPA VVVGFS AALGYRYYGT  
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGV LHV VHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKI QEEYYRLFKNV  
PCCFGCLR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

**N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

**Glycosaminoglycan attachment site.**

amino acids 49-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

**Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

**Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

**N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

**Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## **FIGURE 20**

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGCGAATGTTGCAGTGCATTTATATTATAAGAGTAT  
TGGTCCCTTGCTTCATCATCTGACAACCTTCTTATTGAAACCTCAAAATTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC  
ATTATATGAACTTGAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA  
GGAGTCTATGTGGCATTTGGAATACTCACCTGATACCAGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA  
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTTACCTTC  
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

## **FIGURE 21**

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG  
CTAAGCGAGGCCTCCTCCTCCCGAGATCCGAACGGCCTGGGCGGGTCACCCCGGCTGGGA  
CAAGAAGCCGCCGCTGCCTGCCGGGCCGGGAGGGGGCTGGGCTGGGCGGGAGGCAG  
GGTGTGAGTGGGTGTGTGCGGGGGCGGAGGCTTGATGCAATCCGATAAGAAATGCTCGGG  
TGTCTTGGGCACCTACCGTGGGCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG  
CCGCCGCCGTAGAGCAGGAGCGCTCGCTCAGGATCTAGGGCACGACCATCCAACCC  
GGCACTCACAGCCCCGAGCGCATCCCGTCGCCAGCCTCCGCACCCCCATGCCGG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGC GGAGCGGGTGTGTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCGTGGCGCCGGCGCCCCCTGCCCTCTCGGACGCCGGGCC  
CCACGTGCACTACGGCTGGGCGACCCCATCCGCCTGCCACCTGTACACCTCCGGCCCC  
ACGGGCTCTCCAGCTGCTTCTGCCATCCGTGCCAGGGCGTGGACTGCCGCCGGG  
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTCTGCCACCGTGGCATCAAGGG  
CGTGCACACGGTGCACCTCTGCATGGCGCCGACGGCAAGATGCAGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTCAGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA  
TCCGAGAACGCCCTCCGGCTCCCTGAGCAGTGCCAAACAGCGGAGCTGTACAAGAA  
CAGAGGCTTCTTCACTCTCATTCCGCCTGCCCCATGCTGCCCATGGTCCCAGAGGAGCCTG  
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG  
GACCCATTGGCTTGTCAACGGACTGGAGGCCGTGAGGAGTCCAGCTTGAGAAGTAACT  
GAGACCATGCCGGCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGACG  
TGCTTCTACAAGAACAGTCCCTGAGTCCACGTTCTGTTAGCTTAGGAAGAAACATCTAGAA  
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCCAGTTCTAGCCAATAGACTGTCTGAT  
CATAAACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCCTGGGCCCTATTCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGCTCAGTTCTGCTGAATAACCTCCATCGATGGGAAC  
TCACCTCCTTGGAAAATTCTTATGTCAAGCTGAAATTCTCTAATTCTCATCACTTC  
CCCAGGAGCAGCCAGAACAGGAGTAGTTAATTCAAGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAAATTCACTCAACCCATGTGGAATTGATCTATCTACTTCCAGGG  
ACCATTGCCCTCCCAAATCCCTCCAGGCCAGAACACTGACTGGAGCAGGCATGGCCACCAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGGCCCTGGGACAACCTGAGAATTCCCC  
CTGAGGCCAGTTCTGTCATGGATGCTGCTGAGAATAACTGCTGTCCGGTGCACCTGC  
TTCCATCTCCAGGCCACCAGCCCTGCCCACCTCACATGCCCTCCCATGGATTGGGGCCT  
CCCAGGCCCCCACCCTTATGTCAACCTGCACTCTGTTCAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCCAAGTCTTGTCAATAACTGCTGTGAGCAGGGGGAGACCTAGAAC  
CCTTCCCCAGCACTGGTTTCAACATGATATTATGAGTAATTATTTGATATGTACA  
TCTCTTATTCTTACATTATTATGCCCAAATTATATTATGTATGTAAAGTGAGGTTG  
TTTGTATATTAAAATGGAGTTGTTGT

## **FIGURE 22**

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE  
EIRPDGYNVYRSEKHLRVPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSDMDPFGLVTGLEAVRSPSFEK

**Signal peptide:**

amino acids 1-22

**Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

**N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

## **FIGURE 23**

CCCAGAAGTCAGGGCCCCGGCCTCCTGCCTGCCGCGGGACCCCTGACCTCCTCA  
GAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGGAGGAGCCACCGCTCCTGCTG  
CTGCTGCCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGCCAAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTAGCCTGCAAAACCCAA  
AGAAGACTGTTCTCCAGATTAGAGTGGAGAAACTGGGTGGAGTGTCCTTGTCTAC  
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG  
GATCAAAATGTGACAAGAAGTGTGAGCTGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG  
AGCAAGGCCAAACCTGGAAGAGGATAACAGTCACACTGGAAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGAAATCCAGCTCTGAATAACACATGGTTAAGGATGGCATCCGTTGCTAGAAA  
ATCCCAGACTTGGCTCCAAAGCACCAACAGCTCATACACAATGAATACAAAAACTGGAAC  
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCTGTGAAGCCCGCAATT  
TGTTGGATATCGCAGGTGTCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA  
TCATAGCAGCCGTAGTAGTTGTGGCCTAGTGATTCCGTTGTGGCCTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA  
AGCCACGACAATGAGTGAAATGTGCAGTGGCTCACGCCGTAAATCCCAGCACTTGGAAAGG  
CCGGCGGGCGGATCACGAGGTCAAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAACCC  
CATCTCTACTAAAATACAAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC  
TTGGGAGACAGGAGAATCACTGAACCCGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAATAAAATAATA  
AATAAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

## FIGURE 24

MARRSRHLLLLLRLVVALGYHKAYGFSAPKDJQQVVTAVEYQEAILACKTPKTVSSRLE  
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED  
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGI RLLENPRLGSQST  
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVA  
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAGGSRGQEF

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 130-144, 238-258

**N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

**Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

**N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

**Amidation site.**

amino acids 226-230

## **FIGURE 25**

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGGAGGAGAAAGAG  
AAAGAAGAGGAAGATGTTGGCAACATTATTAAACATGCTCCACAGCCGGACCCCTGGCAT  
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGATTAAATATTACTTCTAAATAA  
ATGAATTACTCAATCTCCTATGACCACACTATACATACTCCACCTCAAAAAGTACATCAATA  
TTATATCATTAAAGGAATAGTAACCTCTCTCCAATATGCATGACATTGGACAATG  
CAATTGTGGCACTGGCACTTATTTCAGTGAAGAAAAACTTGTGGTTCTATGGCATTCA  
TTTGACAAATGCAAGCATCTCCTATCAATCAGCTCTATTGAACTTACTAGCACTGACTG  
TGGAATCCTAAGGGCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT  
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAG  
TGGATTGTCCACGGTTATGTACGTGAAATCAGGCCTGGTTACACCCAGATCCATTAT  
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTCCCAGCCAGATTGCC  
AGCTAACACACAGATTCTCTCCTACAGACTAACAAATATTGCAAAATTGAATACTCCACAG  
ACTTTCCAGTAAACCTACTGGCCTGGATTATCTCAAAACAATTATCTCAGTCACCAAT  
ATTAATGTAAGGAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAACAAACTTACTGA  
ACTGCCTGAAAATGCTGTCGAACACTACAAGAACTCTATATTAAATCACAACT  
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTTCTCGACTTCATCTC  
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT  
TCTGATGATTGGGAAAATCCAATTATCAGAACAGACATGAACTTTAACGCCTTATCA  
ATCTTCGAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCCTGGTT  
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCCATGT  
TGCTCTCAAAAGTGTAAATCTCAAATTGGATCTAAATAAAATCCTATTAAATAGAA  
TACGAAGGGGTGATTTAGCAATATGCTACACTAAAAGAGTTGGGATAAAATAATATGCCT  
GAGCTGATTCCATCGATAGTCTGCTGTGGATAACCTGCCAGATTTAACAAAAATAGAAC  
TACTAACAAACCTAGATTGTCTTACATTCCCCAATGCATTTCAGACTCCCCAAGCTGG  
AATCACTCATGCTAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCTGGTACTCTG  
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTACTGTGTACCCGTTG  
GATGAACATGAACAAAACCAACATTGGATTATGGAGCCAGATTCACTGTTTGCCTGGACC  
CACCTGAATTCCAAGTCAGAACATGTTGGCAAGTGCATTTCAGGGACATGATGGAAATTG  
CTCCCTTCTTATAGCTCTGAGAGCTTCTTCTAAATCTAAATGTAAGAGCTGGGAGCTATGT  
TTCCTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTG  
GTCAAAACTCTGCCTAATACCCCTGACAGACAAGTTCTATGTCCTTCTGAGGGAACACTA  
GATATAATGGCGTAACTCCCCAAGAAGGGGTTATATAACTTGTATAGCAACTAACCTAGT  
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAATG  
GCTCTTGAATATTAAAATAAGAGATATTGGCCAATTCACTGGTGTGTTGCTGGAAAGCA  
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA  
TGCTGCGCAAAGTGCCTGAATACCACATGATGTCAGGTATATAATCTTACTCATCTGAATC  
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTACAGAAAAACAGAAAAAAA  
TGTGTAATGTCACCACCAAGGTTGCACCCCTGATCAAAAAGAGTATGAAAAGAATAATAC  
CACAAACACTTATGGCCTGTCTGGAGGCCTTCTGGGATTATTGGTGTGATATGTCTTATCA  
GCTGCCCTCTCCAGAAATGAACCTGTGATGGTGACACAGCTATGTGAGGAATTACTTACAG  
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGTATAAAATCTCTGGGAAGCAGGAAA  
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCT  
AAAAACCACCAAGGAAACCTACTCCAAAAATGAAC

## **FIGURE 26**

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT  
FPARLPANTQILLQTNNIAKIEYSTDFPVNLTGDLDSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLRLHLNSNRQLQMINSKWFDA  
LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRL  
IKVPHVALQKVNLKFSDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSIAVDNLPD  
LRKIEATNNPRLSYIHPNAFFRLPKLESMLMSNALSALYHTIESLPNLKEISIHSNPIRC  
DCVIRWMNMNKTNIRFMEPDSDLFCVDPPEFQGQNVQVHFRDMMEICLPLIAPESFPSNLNV  
EAGSYVSFHCRTAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC  
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV  
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE  
YEKNNTTTLMACLGGLLGIIGVICLISCLSPEMNCDDGHSYVRNYLQKPTFALGELYPP LIN  
LWEAGKEKSTSLKVKATVIGLPTNMS

**Signal sequence:**

amino acids 1-22

**Transmembrane domain:**

amino acids 633-650

**N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

**Tyrosine kinase phosphorylation site.**

amino acids 570-579

**N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

**Cell attachment sequence.**

amino acids 277-280

## FIGURE 27

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC  
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTATTATGCTGACATTCCAGCATGAATCT  
GGTAGACCTGTGGTTAACCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTGTTCTTA  
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTCTCCTCTGGG  
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG  
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT  
GCCTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAATGCCTCAATAACCTGAAGGCCAGGCCAGAATTGCCAACAAACCCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC  
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC  
CAACGACGCTGACCTTGTAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTGCTGGTCACATGGTGTCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG  
GATGCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGTAAGTGTCCAAACTGACTGTCAATTGAGAAAGAAAGAAA  
GTAGTTGCATTGCAGTAGAAATAAGTGGTTACTTCTCCATCCATTGTAAACATTGAA  
ACTTGTATTCAGTTTTGAATTATGCCACTGCTGAACCTTAACAAACACTACAACA  
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTTT  
AATTAAAAGCAAATAAGCTTAACTTGAACCAGGGAAAAAAAAAAAAAAACA

## **FIGURE 28**

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLSSGGLNVTCSNANLKEIPRDL  
PPETVLLYLDNSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR  
IQSVHKNAFNKLARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFL  
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK  
ADEPDDISTVV

**Signal sequence:**

amino acids 1-33

**Transmembrane domain:**

amino acids 205-220

**N-glycosylation site.**

amino acids 47-51, 94-98

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

**Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

**N-myristoylation site.**

amino acids 37-43, 45-51, 110-116

## **FIGURE 29**

ACCGAGCCGAGCGGACCGAAGGCAGCAGGGATTGCAGGTGAGCAAGAGGATGCTGGCGGG  
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCACCTCCTGCTGGTGCT  
GGGCTCAGTGTCTGGCAGGCTGGCCACGGCTGCCGCCGCTGCGAGTGCTCCGCCAGG  
ACCGCGCTGTGCTGCCACCGCAAGTGCTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG  
ACGCGCCTGCTGGACCTAGGCAAGAACGCATAAAACGCTCAACCAGGACGAGTTCGCCAG  
CTTCCCGCACCTGGAGGAGCTGGAGCTAACGAGAACATCGTGAGCGCCGTGGAGGCCGG  
CCTTCAACAACCTCTAACCTCCGGACGCTGGGTCTCCGCAGCAACGCCCTGAAGCTCATC  
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCAGAAACAAGAT  
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACACTCAAGTCAGTGAGGTTGGCG  
ACAATGACCTCGTCTACATCTCACCGCCTTCAGGGCCTCAACAGCCTGGAGCAGCTG  
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCGTGTCCCACCTGCACGCC  
CATCGTCTGAGGCTCCGGCACCTAACATCAATGCCATCCGGACTACTCCTTAAGAGGC  
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCTACTTGGACACCATGACACCCAAC  
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC  
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCCCTAACCTCTCCTACACCCCCATCA  
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGCG  
GGGAGCTGGCGTGGAGCCCTATGCCTTCCGGCCTCAACTACCTGCGCGTGTCAA  
TGTCTCTGGCAACCAGCTGACCAACACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG  
AGACACTCATCTGGACTCCAACCCGCTGGCCTGCGACTGTCGGCTCTGTGGGTGTTCCGG  
CGCCGCTGGCGCTCAACTTCAACCGCAGCAGGCCACGTGCGGCCACGCCAGTTGTCCA  
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTCACCTGCCGCCGCG  
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTGGACGAGGGCACACGGTGCAGTT  
GTGTGCCGGGCCGATGGCGACCCGCCGCCATCCTCTGGCTCTCACCCGAAAGCACCT  
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT  
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGGGCAACGGGGGGCAACGAC  
TCCATGCCGCCACCTGCATGTGCAGCTACTGCCGACTGGCCCCATCAGCCAAACAA  
GACCTTCGCTTCATCTCAACCAGCCGGCGAGGGAGAGGCCAACAGCACCCGCCACTG  
TGCCTTCCCTCGACATCAAGACCCTCATCATGCCACCACTGGCTTCTCTTTC  
CTGGCGTGTCTCTGCCTGGTGTGCTGTTCTCTGGAGGCCGGCAAGGGCAACAC  
AAAGCACAACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAGGCATCAGCTCCGCC  
ACGGCCCGCAAGTCAACATGAAGATGATATGAGGGCGGGCGGGGGCAGGGACCCCCG  
GGCGGCCGGCAGGGGAAGGGCCTGGTCGCCACCTGCTCACTCTCCAGTCTTCCACCTC  
CTCCCTACCCCTCTACACACGTTCTCTTCTCCCTCCGCCCTCGTCCCTGCTGCCCG  
CCAGCCCTCACCACTGCCCTCTTCTACAGGACCTCAGAAGGCCAGACCTGGGACCCCA  
CCTACACAGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTC  
ATAATTCAATAAAAAGTTACGAACCTTCTGTAACTTGGGTTCAATAATTATGGATTT  
TATGAAAAACTTGAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

## **FIGURE 30**

MQVKRMLAGGVRSMPSPLLACWQPI~~LLV~~LGSQLSGSATGCPPCECSAQDRAVLCHRKF  
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL  
GLRSNRLKLIPLGVFTGLSNLTQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA  
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH  
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFNLNSYNPISTIEGSMLHEL  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSVGNNLETLILDSNPLA  
CDCRLLWVFRRRWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVFPDGTLEVRYAQVQDNGTYL  
CIAANAGGNDSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANESTRATVPFPFDIKTLI  
IATTMGFISFLGVVLFC~~L~~VLLFLWSRGKGNTKH~~N~~IIEYVPRKSDAGISSADAPRKFNMKMI

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 556-578

**N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

**Tyrosine kinase phosphorylation site.**

amino acids 590-598

**N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## FIGURE 31

CCACCGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGGCCCTTCGGTCAAC  
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGCGCCCAGCC  
AGGGAGCCGGCCGGGAAGCGCGATGGGGGCCAGCCGGCCTCGCTCCTGCTCCTGCTCCTGC  
TGTCGCTGCTGGCGCCGGGGCAACCTCTCCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGTCAAGTGCCAAGTGAAGATCA  
CGAGGACTCATCCCTGCAATGGCTAACCTGCTCAGCAGACTCTACTTTGGGGAGAAGA  
GAGCCCTCGAGATAATCGAATTCAAGCTGGTTACCTCTACGCCAACGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTCACTATGCCTGT  
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCACTGGTT  
ATAATCTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTTCTGGGAGCAAG  
CCTGCAGCCGGCTCACCTGGAGAAAGGGTACCAAGAACTCCACGGAGAACCAACCCGCAT  
ACAGGAAGATCCCAATGGTAAAACCTTCACTGTGAGCAGCTCGGTGACATTCCAGGTTACCC  
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCAGTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCCTCGTGAGGGCCAGAACGCTTGTGCTACACTGTGAGGGTCGCGGAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTCCCTTCCCTAACAAAGAGTGAAGTGGCACCTACGGCTGCACAGCCACCA  
CAACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT  
CCTCCTCCAGCACCTACCACGCCATCATCGTGGGATCGTGGCTTCATTGTCTCCTGCTG  
CTCATCATGCTCATCTCCTGGCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA  
TGAGGCAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG  
GGCAGTCAGGAGGGACACAAGGAATATTCATCTAGAGGCGCCTGCCACTCCTGC  
GCCCCCCAGGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA  
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAAATGTCTGC  
TTTGGGTGCGGTTTGTACTCGGTTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGAGGG  
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGGTTATTATTATTGTAAACAATCC  
CAAATCAAATCTGTCCTCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA  
AACAAAAAACAA

## **FIGURE 32**

MGAPAASLLLLLFAACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLKCQVKDHEDSSLQW  
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELYSISISNVALADEGEYTCISIFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

**Signal sequence:**

amino acids 1-20

**Transmembrane domain:**

amino acids 331-352

**N-glycosylation site.**

amino acids 25-29, 290-294

**Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

**N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 33**

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTCTCCTTCCTGG  
CTTCGGACATTGGAGCACTAAATGAACCTGAAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG  
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGTTAAAAATGCTGCTTGGATTCTGTT  
GCTGGAGACGTCTTTGCTTGCCTGGAAACGTTACAGGGGACGTTGCAAAGAGAAGA  
TCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAAAGGGCTTCACA  
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTACCATTATTCATGGCAATTC  
CCTCACTCGACTTTCCATAATGAGTTGCTAACCTTATAATGCGGTTAGTTGCACATGG  
AAAACAATGGCTGATGAAATCGTCCGGGGCTTTCTGGGCTGCAGCTGGTAAAAGG  
CTGCACATCAACAAACAAGATCAAGTCTTTCGAAAGCAGACTTTCTGGGCTGGACGA  
TCTGGAATATCTCCAGGCTGATTTAATTACGAGATATAGACCCGGGGCTTCCAGG  
ACTTGAACAAGCTGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCTT  
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC  
CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC  
CACCGAACAGGACTTGTGTCCTTGAAAAACCGAGTGGATTCTAGTCTCCGGCCCGCCCTG  
CCCAAGAACAGAGACCTTGCTCCTGGACCCCTGCCAACCTTCAAGACAAATGGCAAGAG  
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT  
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC  
GTTTACCCCTGCCCTGGGGCTGAGCTGCGACCACATCCCAGGGTGGTTAAAGATGAAC  
TGCAACAAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCAAGCTCTAACGTGCAGGA  
GCTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTGTGGATTACAAGA  
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACACACTTTCAAG  
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCGGGA  
GAAATTGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA  
TCCTCCGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAAACACCTG  
CTGAGGTCCCTGCCTGTGGACGTGTTGCTGGTCTCGCTCTAAACTCAGCCTGCACAA  
CAATTACTCATGTACCTCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA  
TAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTCAAGCAGTGGGCA  
GAACGCTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTCTT  
TAGAAAGGATTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT  
CGCCCACGTTAACCTCGCACAGTAAAACAGCACTGGGTGGGGAGACCGGGACGCACTCC  
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTGGTGTGGTCCGGACTGCTGCTGGT  
GTTTGTACCTCCGCCTCACCGTGGGGCATGCTCGTGTGTTATCCTGAGGAACCGAAAGC  
GGTCCAAGAGACGAGATGCCAACCTCCCGCGTCCGAGATTAACTCCCTACAGACAGTCTGT  
GAECTTCCCTACTGGCACAATGGGCTTACAACGAGATGGGCCCACAGAGTGTATGACTG  
TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGAGGGCAGAGGGAAAGGG  
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCCGCG  
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTCGCACAAACGAAAGGGCT  
GACCCCTACTTAGCTCCCTCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA  
GCCAGCTCGCTTTGCTGAGAGGCCCTTTGACAGAAAGGCCAGCACGACCCCTGCTGGAAG  
AACTGACAGTGCCCTGCCCTCGGCCCCGGGGCTGTGGGTTGGATGCCCGGTTCTATAC  
ATATATACATATATCACATCTATATAGAGAGATAGATATCTATTTTCCCTGTGGATTAG  
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT  
TGTAAATAAGTAACTTGACTTCTGAC

## **FIGURE 34**

MLLWILLLETSLCFAAGNVTGVCCKEKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH  
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFGLQLVKRLHINNNKIKSFRKQ  
TFLGLDDLEYLQADFNLLRIDPGAFQDLNKLEVILINDNLISTLPANVFQYVPITHLDLRG  
NRLKTLPLYEEVLEQIPIGIAEILLEDPWDCTCDLLSKEWLENIPKNALIGRVVCEAPTRLQ  
GKDINETTEQDLCPLKNRVDSSLPPAPPQAEEFTAPGPLPTPKTNGQEDHATPGSAPNGGT  
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSDHIPGSGLKMNCNNRNVSSLADLKP  
KLSNVQELFLRDNIHSIRKSHFDYKNLILLLDGNNNIATVENNTFKNLLDLRWLYMDSNY  
LDTLSREKFAGLQNLEYLNVEYNIAIQILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL  
SKLSLHNHYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC  
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHNSYLDTSRVSISVL  
VPGLLLVFVTSRAFTVGMLVFILENRKRSKRRDANSASEINSLQTVCDSYWHNGPYNADG  
AHRVYDCGSHSLSD

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 618-638

**N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

**Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

**N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

## **FIGURE 35**

AGTCGACTGCGTCCCTGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC  
TGCACCGGGCCTGGCAGCGCTCCGCACACATTCTGTGCGGGCTAAGGGAAACTGTTGGC  
CGCTGGGCCCGGGGGATTCTTGGCAGTTGGGGTCCGTGGGAGCGAGGGCGGAGGGG  
AAGGGAGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC  
AGCTCTGCGTCCTCGAGCGGACAGATCCAAGTTGGGAGCAGCTGTGCGTGCAGGGCCTCAG  
**AGAATGAGGCCGGCGTTCGCCCTGTGCCCTCTGGCAGGCCTCTGGCCCGGGCGG**  
CGGCGAACACCCCCACTGCCGACCGTGTGGCTGCTCGGCCCTGGGGCCTGCTACAGCCTGC  
ACCAAGCTACCATGAAGCGGCAGGGCGGAGGAGGCTGCATCTGCGAGGTGGGGCGCTC  
AGCACCGTGCCTGCAGCTCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCAGG  
GCCCGGAGGGGCTCAAAGACCTGCTGTTCTGGTGCAGTGAGCGCAGGCCTTCCACT  
GCACCCCTGGAGAACGAGCTTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACC  
GAAAGCGACACGCTGCAGTGGGTGGAGGAGATGCCACCTGC  
GGTACTCCAGGCCACCGGTGGGTGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC  
GCGCCAACGGCTACCTGTGCAAGTACCAAGTTGAGGTCTGTGCTCGCCGCCCGGG  
GCCGCCTCTAACTTGAGCTATCGCGCCCTTCCAGCTGCACAGCGCCCTGGACTTCAG  
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTTGCA  
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTCGGGCGATGTGTTGTGCCCTGCC  
GGGAGGTACCTCCGTGCTGGCAAATGCGAGAGCTCCCTAACTGCCCTAGACGACTTGGGAGG  
CTTGCCTGCGAATGTGCTACGGCTTGCAGCTGGGAAGGACGGCCGCTTGTGACCA  
GTGGGGAGGACAGCCGACCCCTGGGGGACGGGGTGCCACCAGGCCCGCCGGCCACT  
GCAACCAGCCCCGTGCCGAGAGAACATGGCAAATCAGGGTCGACGAGAACGACTGGGAGAGAC  
ACCACTGTCCTGAACAAGACAATTCAAGTAACATCTATTCTGAGATTCTCGATGGGAT  
CACAGAGCACGATGTCTACCCCTCAAATGTCCCTCAAGCCGAGTCAGGCCACTATCACC  
CCATCAGGGAGCGTGATTCCAAGTTAATTCTACGACTCCTCTGCCACTCCTCAGGCTT  
CGACTCCTCCTCTGCCGTGGTCTTCATATTGTGAGCACAGCAGTAGTAGTGTGTTGATCT  
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTACGAAAGCCCTTCCAGCCA  
AGGAAGGAGTCTATGGGCCGCCGGCTGGAGAGTGATCCTGAGCCGCTGCTTGGCTC  
CAGTTCTGCACATTGCACAAACAATGGGTGAAAGTCGGGACTGTGATCTGCCGGACAGAG  
CAGAGGGTGCCTTGTGGGGAGTCCCTTGGCTCTAGTGATGCATAGGGAAACAGGGGA  
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTAC  
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCCTCTAAATTCCCTTACTCCACTGAG  
GAGCTAAATCAGAACACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA  
TGGTGTGATAGTGGGGACCGGGTAGTGTGGGAGAGATATTCTTATGTTATTGGAGAA  
TTTGGAGAAGTGATTGAACCTTCAAGACATTGGAAACAAATAGAACACAATATAATTACA  
TTAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT  
ATTGGTTGAAATCCCAGGGAAAAAAATAAAAATAAAGGATTGTTGAT

## FIGURE 36

MRPAFALCLLWQALWP GP GGG EHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS  
TVRAGAELRAVLALLRAGPGP GGG SKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGLE  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPGA  
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGFFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA  
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILTMVLGLVKLCFHESPSSQPR  
KESMGPPGLES DPEPAALGSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 189-193, 381-385

**Glycosaminoglycan attachment site.**

amino acids 289-293

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

**Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

**N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## **FIGURE 37**

CGGACGCGTGGGATTCAAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG  
CGTCGAGTCAGACGGCACCATATAATGCCCTTAAAAGTGCCTCCGCCCTGCCGGCGTATC  
CCCCGGCTACCTGGGCCCGCCCCCGCGCGGTGCGCGCTGAGAGGGAGCGCGCAGCGA  
GGGCCGGTGTGAGCCAGCGCTGCCAGTGTGAGCGGGCGGTGAGCGCGGTGGTGCAGCGA  
GGGGCGTGTGAGCCAGCGCTGCCAGTGTGAGCGGGCGGTGAGCGCGGTGGTGCAGCGA  
GGGGCGCGAACGCCCTGGCGCCACTCTGCCCTGCTGCTGCCGCCACCCAGCTCTCGCGG  
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTACTGGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTTCCCTGGAGTGACCCCTCAAATAGCAAATGTACTGGAAAATCA  
CAGTTCCGAAGGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC  
CTGTGCCGCTATGACTTGTGGATGTGTACAATGCCATGCCATGCCAGCGCATTGGCCG  
CTTCTGTGGCACTTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGCCATGTTCTCCGCTGTAACCA  
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAAAC  
CCCCAAGTGGCCAGACCGGGATTACCCCTGCAAGGAGTCATTGTGTGGCACATTGAGCCC  
CAAAGAATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTAATGCCGGGAAGTCAACGATGCTAGAAGAATTGGAAA  
GTATTGTGGTGTAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTCTTATTCACT  
TTTATCAGACTTAAGTTAACTGCAGATGGTTATTGGTCACTACATATTAGGCCAAA  
AAACTGCCTACAACACAGAACAGCCTGTCACCACACATTCCCTGTAACCACGGGTTAAA  
ACCCACCGTGGCCTGTGTCACACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT  
GTTCAAGTGACTTGTATTAGCCGGCACTGTTACACAAACATCACTCGCGATGGAGTTG  
CACGCCACAGTCTGATCATCAACATCTACAAAGAGGGAAATTGGCGATTAGCAGCAGCGGG  
CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCTCTCCTCAGAACAGGTC  
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGCAAATCATGCCAACAGC  
TTTATCATGATGTTCAAGACCAAGAACATAGAACAGCTCTGGATGCCCTAAAAATAAGCAATG  
**TAA**ACTGAACTGTGTCATTAAAGCTGTATTCTGCCATTGCCCTTGAAGAGATCTATGTT  
TCTCAGTAGAAAAAAACTTATAAAATTACATATTCTGAAAGAGGATCCGAAAGAGATGG  
GACTGGTTGACTCTCACATGATGGAGGTATGAGGCCCTCGAGATAGCTGAGGGAAAGTTCT  
TGCCTGCTGTCAAGAGGAGCAGCTATGATTGGAAACCTGCCGACTTAGTGCAGGTGATAGGA  
AGCTAAAAGTGTCAAGCGTTGACAGCTGGAAAGCGTTATTATACATCTCTGTAAGGAT  
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTAGAAGTGCATATTATAGT  
GTTATTGTTCACCTCAAGCCTTGCCCTGAGGTGTTACAATCTGTCTGCAGTTCTA  
AATCAATGCTTAATAAAATATTAAAGGAAAAAA

## FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDYDYPAGVTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI  
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRTGTLEGN  
YCSSDFVLAGTVITTITRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR  
GLNYIIMQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

**Signal sequence:**

amino acids 1-23

**N-glycosylation site.**

amino acids 355-359

**Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

**Tyrosine kinase phosphorylation site.**

amino acids 199-208

**N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

**Cell attachment sequence.**

amino acids 149-152

## **FIGURE 39**

CGGACGCGTGGCGGACGCGTGGCGCCACGGCGCCGCGGCTGGGCGGTGCTTCTT  
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCCAGGACCTATCTGG  
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTACACTG  
CCGGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACCATCCGGGACAACCTTGAG  
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG  
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTCGAGTGCCACCGCCTGGAGCT  
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTTTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCTGC  
CTTCCCTGTCTGGGGAACAGAGAGAGGCCCTGCGGTGGCTACGGCAGTGTGAAGGAGAAGG  
GACACGAGGGGGCAGCGGCAGTGTGACTGCCAAGCCGGCTACGGGGTGAGGCCTGTGGCC  
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT  
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGTTGCAATGCAAGAAGGG  
CTGGGCCCTGCATCACCTCAAGTGTGAGACATTGATGAGTGTGGCACAGAGGGAGCCA  
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCTAGGCTGCATGGGGCAGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGAGAGA  
ACAAGCAGTGTGAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGCAGCAGATGTTCTTGGCATCATCATCTGTGCACTGGCCA  
CGCTGGCTGCTAAGGGCAGCTGGTGTACCCGCATCTCATTGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTTGTCAAGAGCAGTGCAGCGACTGGCTGGAGGGCTTCATCAAGGGCAGATA  
ATCGCGGCCACCACCTGTAGGACCTCTCCCACCCACGCTGCCCGAGAGCTTGGCTGCC  
TCCTGCTGGACACTCAGGACAGCTGGTTATTTGAGAGTGGGTAAGCACCCTACCTG  
CCTTACAGAGCAGCCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC  
CCTGAAGGTGGATACCATGAGCTCTCACCTGGCGGGACTGGCAGGCTTCACAATGTGTGA  
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG  
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCTGCCAGTTCTGT  
TCTGTGTTCACACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAGA  
AAGGTCTTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 40

MAPWPPKGVLPAVLWGLSLFLNLPGPIWLQPSPPPQS PPPQPHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLESELVESWWFHKQ  
QEAPDLFQWLCSDSLKLCGPAGTFGPSCLPCCPGTERPCGGYGCCEGEGRGGSGHCDCQAG  
YGGEACGQCGLGYFEAERNASHLVCACFGPCARCSGPPEESNCLQCKKGWALHHLKCVDIDE  
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKCSPGYQQVGSKCLDVDECE  
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG  
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

**Signal sequence:**

amino acids 1-29

**Transmembrane domain:**

amino acids 372-395

**N-glycosylation site.**

amino acids 79-83, 205-209

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

**Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

**N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

**Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

**EGF-like domain cysteine pattern signature.**

amino acids 181-193

## **FIGURE 41**

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA  
GCACCATGCAGCCCCGTGGCTCTGCTGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG  
GCCGCCCTGACCAGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTGCAGCTCAAAGAGGT  
GCCCACCCCTGGACAGGGCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT  
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTAGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTCGG  
CATGGAGCAGCGCTGCCGCCAACAGCGAGCTGGTCAGGCCGTGCTGCCGTCTCCAGG  
AGCCGGTCCCCAAGGCCGCGTGCACAGGCACGGCGGCTGTCCCCGCGCAGGCCCGGGCC  
CGGGTGACCGTCGAGTGGCTGCGCGTCCCGACAGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTCAGAGG  
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGGC  
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG  
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGATGAAGTGGGCCGAGAACTGGGTGCTGGAGCCCCCGGGCTT  
CCTGGCTTATGAGTGTGGCACCTGCCGGCAGCCCCCGGAGGCCCTGGCCTTAAGTGGC  
CGTTTCTGGGCCTCGACAGTCATGCCCTGGAGACTGACTCGCTGCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA  
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCAAGGAGGCTCAGCCATAGGCGCCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGGTGCAGGGTACCAAGGAGAGCTG  
GCGATGACTGAACCTGCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT  
CCTCTGACAAGTTACCTCACCTAATTTGCTCTCAGGAATGAGAATCTTGGCCACTGGA  
GAGCCCTGCTCAGTTCTCTATTCTACTGCACATATTCTAAGCACTTACAT  
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCATTGTTACTTGTCCGTAC  
TGGATCTGGCTAAAGTCCTCCACCACCACTCTGGACCTAACAGACCTGGGTTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAATAAGACTTTGAAAACATGAATAAAACACATTATTCT  
AAAA

## FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLRLQLKEVPTLDRADMEELVIPTHVRAQYV  
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP  
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF  
WQQLSRPRQPLLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF  
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 158-162

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

**Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

**N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

**Amidation site.**

amino acids 74-78

**TGF-beta family signature.**

amino acids 282-298

## **FIGURE 43**

GTCTGTTCCCAGGAGTCCTCGCGGCTGTTGTCAGTGGCCTGATCGCGATGGGACAAA  
GGCGCAAGTCGAGAGGAAACTGTTGTCCTCTCATATTGGCGATCCTGTTGCTCCCTGG  
CATTGGGCAGTGTACAGTGCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT  
GTGAAGTTGTCCTGTCCTACTCGGGCTTTCTTCTCCCCGTGGAGTGGAGTTGACCA  
AGGAGACACCACCACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG  
TGACCTTCTGCCAACCTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTGCCACCATTGGGAACCGGG  
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTCTGAATAACACCTGGTCAAAGAT  
GGGATAGTGTGCTACGAATCCAAAAGCACCCGTGCCTTCAGCAACTCTCCTATGTCT  
GAATCCCACACAGGAGAGCTGGTCTTGATCCCCTGTCAAGCTCTGATAACTGGAGAACACA  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGATGGAGCT  
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCCCTGATTCTCCTGGGAAT  
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAACCAAACAG  
ACCTCGTCATTCTGGTGTGACCTGGTCGGCTACCGCCTATCATCTGCATTTGCCTTACT  
CAGGTGCTACGGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCATTGTCTTC  
TACACCCCACAGGGCCCCCTACTTCTGGATGTGTTTAATAATGTCAGCTATGTGCC  
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACCTGTTAAA  
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGCAAAATGGCGGGGTGCGAGGAATCTGCACTCAACTGCCACCTGGC  
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTTCTGGCTCTTCCTGTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG  
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTGTCTTCCATGGGAAGTG  
CCACTGGATCCCTCTGCCCTGTCCCTGAATACAAGCTGACTGACATTGACTGTCTGT  
GGAAAATGGGAGCTTGTGGAGAGCATAGTAAATTCAGAGAACCTGAAGCCAAAAG  
GATTAAAACCGCTGCTCTAAAGAAAAGAAAATGGAGGCTGGCGCAGTGGCTACGCCTG  
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGAGTTGGATCAGCCTGACCA  
ACATGGAGAACCCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAGAGCAAAACTCCAGCTCAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRI PENNPVKLSCAYSGFSSPRVEW  
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGYTCMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNIPSSATIGNRAVLTSEQDGSPPSEYTWFKDGI VMPTNPKSTRAFSNS  
SYVLNPTTGEELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGFKQTSSFLV

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

## FIGURE 45

CAGCGCGTGGCCGGCGCCGTGTTGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA  
GCGTGGCGAACAGGGCTCTGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCT  
GGAGGCCGCCGAGCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG  
GCTCGTGCCACCCACCAAGTTCCAGTGCCGCACCAGTGGTTATGCGTGCCCCCACCTGG  
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCAACCGCCCCCTGGCCTCCCCTGCCCTGCACCGCGTCA  
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA  
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCACTCACGTGGCGCTGCGACGGCCA  
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCGGAAG  
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC  
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTCGGAATGCCACATCCTC  
CTCTGCCGGAGACCAGTCTGGAAGCCAACTGCCTATGGGTTATTGCAGCTGCTGCGGTGC  
TCAGTGCAAGCCTGGTCACCGCCACCCCTCCTCTTTGTCCTGGCTCCGAGCCAGGAGCGC  
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAACAGAC  
CTCGCTGCCTGAGGACAAGCAACTGCCACCGTCACTCACGCCCTGGCGTAGCCGGACA  
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACAGAC  
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGCCCTGTGCTTAAGAACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

## **FIGURE 46**

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCRDLDCCSDGSDEEECRIEPCTQKGQC PPPPGLPCPCTGVSDCSGGTDKKL  
RNCSRLA CLAGELRCTL SDDCIPLTWRCDGHPDCPDSSDELCGGTNEILPEGDATTMGPPVT  
LESVTSLRNATTM GPPVTLES VPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL  
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

**Signal sequence:**

amino acids 1-30

**Transmembrane domain:**

amino acids 230-246

**N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

**Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

**N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

**Leucine zipper pattern.**

amino acids 17-39

## FIGURE 47

CCACCGCGTCCGGCTCGCTCGCGCAGCGGCGGAGCAGAGGTGCACAGATGCC  
GTTAGACTGGCGGGGGAGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA  
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGAAATGAACCCGAGCAATG  
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTG  
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGCCCTGCACAGCTCACGGCGGGTT  
CGATGACCTCAAGTGTGCTGACCCGGCATTCCGAGAATGGCTTCAGGACCCCCAGCG  
GAGGGGTTTCTTGAGGCTCTGTAGCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCCTAGGCTGGATCCAAGTGA  
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA  
ACAAGACATATAGACATGGAGAGAACGTAATCATCACTTGTATGAAGGATTCAAGATCCGG  
TACCCCGACCTACACAATATGGTTTCATTATGTCGCGATGATGGAACGTGGAATAATCTGCC  
CATCTGTCAAGGCTGCCCTGAGACCTCTAGCCTTTCTAATGGCTATGTAAACATCTCTGAGC  
TCCAGACCTCCTCCCGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT  
GATGGGTCTGCGTATCTGAGTGCTTACAAAACCTTATCTGGCGTCCAGCCCACCCGGTG  
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCAAATGGTAGTCACGGAGATTCTGTCT  
GCCACCCGCGGCCCTGTGAGCGCTACAACCACCGAACTGTGGTAGTTACTGCGATCCT  
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGTTCTTC  
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA  
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGGTGCTGCTCGTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCTCCCCGGAG  
TTCCAGCAGTGACCCCTGACTTGTGGTAGACGGCGTGCCTCATGCCCTCTGTGGCCAG  
ACGAAGCTGTGAGTGGCGCTTGAGTGCTTAGGCCCGGTACATGCCCTCTGTGGCCAG  
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATAACCCGGCTCAGGGACACGGA  
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTGAGCTGCTCCAAA  
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCTGCTGGACAACCTGACATA  
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATGCCACTGGGT  
GTTGTTCTAAGAAACTGATTGATTAAAAAATTCCAAAGTGTCTGAAGTGTCTTTCAA  
ATACATGTTGATCTGTGGAGTTGATTCTTCTCTGGTTTAGACAAATGTAAACAA  
AGCTCTGATCCTAAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTGATCAAGTC  
CTGTTCTTCTTGACACAGACTGATTAAAATTAAAAGNAAAAAA

## FIGURE 48

MYHGMNPSNGDGFLEQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGVFFEGSVARFHQCQDGFKLKGAHKRLCLHFNGTLGWI PSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMSLCRDDGTWNNLPICQGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS  
VSGSSELLQSLYSPPRCQESTHPASDNPDI IASTAEEVASTSPGIHHAHWVLFLRN

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 325-344

**N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

**Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

**N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

## FIGURE 49

CCCACGCGTCCGCTCCGC~~CC~~CTCCCCCGCCTCCCGTGC~~GG~~TCCGTGGCCTAGAGA  
TGCTGCTGCCCGGTTGCAGTTGTCGCGCACGCCTCTGCCCGCCAGCCGCTCCACCGCCGT  
AGCGCCCGAGTGT~~GGGGGG~~CGCACCCGAGTCGGGCCATGAGGCCGGAACCGCC~~T~~ACAGG  
CCGTGCTGCCGTGCTGGTGGGCTGCCGCCGACGGGTCGCC~~T~~GCTGAGT~~GC~~C  
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCC~~T~~TTGTTA  
TAAAGTCATTACTTCATGATACTTCTGAAGACTGAAC~~TT~~GAGGAAGCCAAGAACGCCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAA~~CT~~GATAGAA  
AAGTTCA~~T~~GGAAAACCTCTGCCATCTGATGGT~~GACTT~~CTGGATTGGCTCAGGAGGCGTGA  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGAC~~CTT~~TATGCTGGACTGATGGCAGCATAT  
CACAATTTAGGA~~A~~CTGGTATGTGGATGAGCCGT~~CCT~~GC~~GG~~CAGCGAGGTCTGCC~~T~~GGTCATG  
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCC~~CT~~ACATGTTCCAGT~~GGA~~ATGATGA  
CCGGTGCAACATGAAGAACAA~~TT~~CATTGCAA~~AT~~ATTCTGATGAGAACACCAGCAGT~~CC~~TT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACAC~~CT~~TACTTCCAGAAGAACACAG  
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAACG~~CT~~GCCTGAATCTGCC~~T~~ACAT  
CCTAATCCCCAGCATT~~CCC~~CTCTCCTCCT~~CC~~TTGTGGT~~CACCAC~~AGTTGTAT~~TT~~GGTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGAC~~CC~~CTAGCACAAAGAACACACC~~ATC~~  
TGGCC~~CT~~CTCCTCACCAGGAAACAGCCGGAC~~T~~AGAGGT~~T~~ACAAT~~TC~~CATAAGAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGAC~~CT~~TGAAGAAT~~TT~~TCA~~CC~~GAGTGT~~TT~~  
CGGGAGAAGCCACT~~CC~~CGATGACATGT~~CTT~~GT~~ACT~~ATGACAACATGGCTGTGAACCC~~ATC~~  
GAAAGTGGTTGT~~GACT~~CTGGT~~GAGCGT~~GGAGAGT~~GG~~ATT~~GT~~GACCAATGAC~~AT~~TATGA  
GTTCT~~CCC~~CAGAC~~AA~~ATGGGAGGAGTAAGGAGT~~CT~~GGATGGT~~GG~~AAAATGAAATATATG  
GTTATTAGGACATATAAA~~AA~~ACTGAA~~AC~~TGACAACAA~~AT~~GGAAAAGAA~~AT~~GATAAGC~~AA~~ATC  
CTCTTAT~~TT~~TCTATAAGGAAA~~AT~~ACACAGAAGGT~~T~~ATGAACAAGCTTAGATCAGGT~~CCT~~GT  
GGATGAGCATGTGGT~~CCCC~~ACGAC~~CT~~C~~T~~GGAC~~CCCC~~ACGTT~~GG~~CTGTAT~~CCTT~~TAT  
CCCAGCCAGTCATCCAGCTCGAC~~CT~~TATGAGAAGGT~~AC~~CTGCCAGGT~~CT~~GGCACATAGTA  
GAGTCTCAATAATGTCACT~~GG~~TTGGTTGT~~T~~ATCTAAC~~TT~~TAAGGGACAGAGCTTAC~~CT~~G  
GCAGTGATAAAAGATGGGCTGTGGAGCTGGAAAACCAC~~CT~~CTGTT~~TT~~CC~~T~~GCTCTATACAG  
CAGCACATATTATCATACAGACAGAAA~~AT~~CCAGAAT~~TT~~CAAAGCCCACATATGGTAGCACAG  
GTTGGC~~CT~~GTGCATGGCAATTCTCATATCTGTT~~TT~~CAAAGAATAAA~~AT~~CAAATAAAGA  
GCAGGAAAAAA

## FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGQTQRPCYKVIYFHDTSRRL  
NFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDL  
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY  
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKTFKESREAALNAYILIPSIPLLLL  
VTTVVCWWICRKRKREQPDNSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL  
KNISFRVCSGEATPDDMSCDYDNMAVNPSFGVTLVSVESGFVTNDIYEFSQDQMGRSKES  
GWVENEIYGY

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 117-121, 312-316

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

**Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

**N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## **FIGURE 51**

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGAGAAGACTTGT  
GTTTCGCTCCTGCAGCCTAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCATGGTGT  
GTTCAGCATGCGCTTGTGGACCCCAGTGGCGTCCCTGACCTCGCTGGCGTACTGCCCTGCACC  
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGCCAGTGTCCGGTCACCGCAGC  
CTGCTGAAGTTGAAAATGGTGCAGGT~~CGT~~GTTCGACACGGGGCTCGGAGTCCTCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC  
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATAATTCTCCTTACGACTCT  
CAATACCATGAGACCACCC~~T~~GAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGGCAT  
GCAGCAAATGTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAAGACATTCCCTTC  
TTTCACCAACCTCAACCCACAGGAGGT~~CTT~~ATT~~C~~GGTCCACTAACATTTCGGAATCTG  
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGT~~C~~AGAAAGAAGGACCCATCATCAT  
CCACACTGATGAAGCAGATT~~C~~AGAAGT~~CTT~~GTAT~~CC~~AACTACCAAAAGCTGCTGGAGCCTGA  
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG  
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGT~~G~~ATAAAAGTGGACTTCTTCATCCTCCT  
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAAGCTGCCCATGCTGAAGAGATTG  
CACGGATGATCGAACAGAGAGACTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCATT~~C~~CCACATCCTAGAGAGCAAC~~T~~GCTGAAAGC  
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG  
TGACCTTCATACCGCTTTAATGACCC~~T~~GGGATT~~TTT~~GACCACAAATGCCACCGTTGCT  
GTTGACCTGACCATGGAAC~~TT~~TACCAGCACCTGGAAATCTAAGGAGTGGTTGTGCAGCTCTA  
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT  
TCTTGAATGCCATGTCAGTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT  
TTAAAATAAGTGCCTTATACAATG

## FIGURE 52

MITGVFSMRLWTPVGVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNQEVFIRSTNIFRNLESTRCLLAGLFQCQKE  
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRQTAISLQPGISEDLKKVKDRMGIDSSDKVD  
FFILLDNVAEQAHLNPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLILES  
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMEYLQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## **FIGURE 53**

CTCCTCTAACATACTTGCAGCTAAACTAAATATTGCTGCTGGGGACCTCCTTAGCCT  
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGC~~GG~~CTGGTGGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGACC~~G~~TGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGAGCTGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTGTATGAGCCACCAGCAGAAAAAGAGCAAAGGT~~C~~TCATCCA  
ATCAGTCAGTTGCACAGGAACAGAAGATA~~C~~ATTGGCTCAGTGTGAGCAAGAAGAAGTTATG  
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCCA  
GTCCCAGAGGGTGT~~C~~AGGCTGGCTGACGGCCCTGGCATTGCAAGGGAC~~G~~CGT~~G~~GAAGT~~G~~A  
GCACCAGAACCA~~G~~GTGGTACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGAAAGGTGG  
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGT~~C~~ATGCTCAGGACGAGAAGCAACC~~T~~TC  
GGATTGCC~~C~~TTCTGGGC~~C~~TTGGGGAAAGAACAC~~C~~TGCAACC~~A~~TGATGAAGACACGTGGTCG  
AATGTGAAGATCC~~C~~TTGACTGAGACTAGTAGGAGGAGACAA~~C~~CTCTGCTCTGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTCTGTGATGACA~~A~~CTGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCCCTC~~C~~TCAGAGACCGGA  
AATGCTATGCC~~C~~CTGGGTTGGCCG~~C~~ATCTGGCTGGATAATGTC~~G~~TCAGGGAGGAG  
CAGTCCCTGGAGCAGTGC~~C~~AGCACAGATT~~T~~GGGGTTTCACGACTGCACCCACCAGGAAGA  
TGTGGCTGT~~C~~ATCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA  
GAAAAACACAGAACAGAACGGAGCATTACTGTCTACATGACTGCATGGGATGAACACTGATCT  
TCTTCTGCC~~C~~TTGGACTGGACTTATACTTGGT~~G~~CCCTGATTCTCAGGC~~C~~TTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGA~~A~~CTACATCA  
CCACCTTC~~C~~TATGTCTCCACATTGCACACAGCAGATTCCCAGC~~C~~CTCCATAATTGTGT~~T~~  
CAACTACTAAATACATTCTCACACACACACACACACACACACACACACACATA  
CACCA~~T~~TGTC~~C~~TGTTCTGAAAGAA~~C~~CTGACAAAATACAGATT~~T~~GGTACTGAAAGAGA  
TTCTAGAGGAAC~~G~~GAATT~~T~~AAGGATAAATT~~T~~CTGAATTGGTTATGGGTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTCTGGTAAC~~T~~TATT~~T~~ACAATAATAAGATAGC~~A~~  
TATGTGTT~~C~~AA

## FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGHLRCEGRVEEQKGQWGTVCDDGWDIKDVAVL  
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC  
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPDFDLRLVG  
GDNLCSGRLEVHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIDL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

**Signal sequence:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

**N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

**Amidation site.**

amino acids 196-200

**Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTGACCTCGAC  
CCACCGCGTCCCGGGACCGCGTGGCGGACCGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCCTGGG  
CGTCTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAAGGCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT  
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAAATGGTGGGCCCTAGAACAGCTCATCAGAGA  
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGCCATAGTTGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC  
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACACCACAGTGG  
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCCAGTGCTCTAACGAAAGCACTCC  
TGCCCTCCATGATCAAGAGGGAGGAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTG  
CTGTCTCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTGTAAATGCCATCACCGCGATGGATCTAGGTATGGAGTTATGGAC  
ACCACACAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGTGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTAAGCAGCTGCCTTGGCTGTTATCTTC  
CTCTGGCTCCTGGCTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC  
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAACAGCAGCACTCTTAGGCTTGC  
TTACTCTACAAGGGACAGTTGCATTGAGACTTTAATGGAGATTGCTCTACAAGTGG  
AAAGACTGAAGAAACACATCTGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA  
AGCTTCTCCCAGGGTGAGGGAAACACTTAAGGAATAATATGGAGCTGGGTTAACACT  
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAGGGCGGCCGCACTCTAG  
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGGTTATTGCAGCTTATAATGGTTAC

## FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVTGATSGLGKECAKVFYAAGA  
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI  
VAAAEEILQCFGYVDIL  
VNNAGISYRGTIMDTTVVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI  
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT  
AQGRSPVEVAQDVLAAVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKSNS

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 104-120, 278-292

**N-glycosylation site.**

amino acids 228-232

**Glycosaminoglycan attachment site.**

amino acids 47-51

**Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

**Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

**N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

**Amidation site.**

amino acids 265-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17

## FIGURE 57

CCACCGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTAGAGTGGTAAAAAA  
AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTCTCTGGACATCCTC  
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTATTCTAA  
GAGGAGAAAATCAGTCACCGCGAAATCGTGCTGATTACAGGAGCTGGCATGGAATTGGGA  
GACTCGACTGCCATGAATTGCTAAACTAAAAGCAAGCTGGTCTCTGGATAAATAAG  
CATGGACTGGAGAACAGCTGCCAATGCAAGGACTGGTGCCAGGTTCATACCTTGT  
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
GAGATGTTAGTATTTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA  
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGCACATTCTGGACTACAAA  
GGCATTCTCCTGCAATGACGAAGAATAACCACCATGGCCATATTGTCACTGTGGCTTCGGCAG  
CTGGACATGTCTCGTCCCCTCTTACTGGCTACTGTTCAAGCAAGTTGCTGTTGGA  
TTTCATAAAACTTGACAGATGAACTGGCTGCCTACAAATAACTGGAGTCAAAACACATG  
TCTGTGTCCTAATTCGTAACACTGGCTTCATCAAAATCCAAGTACAAGTTGGACCCA  
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG  
ATTTTATTCCATCTCTATAGCTTTTAACAACATTGGAAAGGATCCTCCTGAGCGTTT  
CCTGGCAGTTAAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA  
AAGCGCAAAGCACCTAGTTCTGAAAACTGATTACCAGGGTTAGGTTGATGTCATCTA  
ATAGTGCAGAATTTAATGTTGAACTTCTGTTTTCTAATTATCCCCATTCTCAATA  
TCATTTTGAGGCTTGGCAGTCTCATTACTACCAACTGTTCTTAGCCAAAAGCTGATT  
ACATATGATATAAACAGAGAAACCTTAGAGGTGACTTAAGGAAAATGAAGAAAAAGAA  
CCAAAATGACTTTATTAAAATAATTCCAAGATTATTGATGGCTCACCTGAAGGCTTGCAA  
AATTGTACCATAACCGTTATTAAACATATATTTTATTGATTGACTAAATTGTT  
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTCAAGCTCTCTAAATAAAA  
TGAAGGACTATATCTAGGGTATTCAACAATGAATATCATGAACTCTCAATGGTAGGTT  
ATCCTACCCATTGCCACTCTGTTCCTGAGAGATACCTCACATTCAATGCCAAACATTCT  
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCATGGGATTAAAG  
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA  
AA  
AA

## FIGURE 58

MKFLLDILLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSI  
LVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVS  
VPFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTS  
LGPTLEPEEVVNRLMH  
GILTEQKMI FIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

**Signal sequence:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34, 283-287

**Casein kinase II phosphorylation site.**

amino acids 52-56, 95-99, 198-202, 267-271

**N-myristoylation site.**

amino acids 43-49, 72-78, 122-128, 210-216

## FIGURE 59

CCACCGCGTCCGGACCGTGGGCGACTAGTTAGATCGCGAGCGGCCGCCGCGCTC  
AGGGAGGAGCACCGACTGCGCCGCACCCCTGAGAGA**ATG**TTGGTGCCTAGTGGAAAGGTGATTG  
TTTCGCTGGTCTGTTGATGCCCTGGCCCTGTGATGGGCTGTTCGCTCCCTACAGAAGT  
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTTCCTCACCCCTTACATTGAAGC  
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTCCGGCCCTTCCCAGGACTGAACATGA  
AGAGTTATGCCGGCTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTGGTTC  
TTCCCAGCTCAGATACAGCCAGAAGATGCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG  
AGGTTCATCCATGTTGGACTCTTGGAACATGGCCTTATGTTGTCACAAGTAACATGA  
CCTTGCCTGACAGAGACTTCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA  
GTGGGCACAGGCTTCAGTTTACTGATGATAACCCACGGATATGCAGTCATGAGGACGATGT  
AGCACGGGATTATACAGTGCACAAATTCAAGTTTCAGATATTCCTGAATATAAAAATA  
ATGACTTTATGTCACTGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC  
ATCCATTCCCTCAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA  
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGCAGAAATTCTGTACCAAATTGGCT  
TGTTGGATGAGAACAAAAAGTACTTCCAGAAGCAGTGCATGAATGCATAGAACACATC  
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCAGCTAAC  
AAAGTGCATCCTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCCTG  
GCACGGAACCTGAGGATCAGCTTACTATGAAATTGGTCACTCCCAGAGGTGAGACAA  
GCCATCCACGTGGGAATCAGACTTTAATGATGAACTATAGTTGAAAGTACTTGCAGA  
AGATACAGTACAGTCAGTTAACCCATGGTTAAGTGAATCATGAATAATTAAAGGTTCTGA  
TCTACAATGCCAAGTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCTGATGGC  
ATGGACTGGAAAGGATCCCAGGAATACAAGAACGGAGAAAAAAAGTTGGAAGATCTTAA  
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAAATTATTC  
GAGGTGGAGGACATATTTACCTATGACCAGCCTCTGAGAGCTTTGACATGATTAATCGA  
TTCATTTATGAAAAGGATGGATCCTTATGTTG**GATAAA**ACTACCTCCAAAAGAGAACAT  
CAGAGGTTTCATTGCTGAAAAGAAAATCGAAAAACAGAAAATGTCATAGGAATAAAAAAA  
TTATCTTTCATATCTGCAAGATTTTCTCATCAATAAAAATTATCCTGAAACAAGTGAGC  
TTTGTTTTGGGGGAGATGTTACTACAAATTAAACATGAGTACATGAGTAAGAATTACA  
TTATTTAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAAGATGTATAATGA  
AATTTCAGGGTCTTGAATAGGAAGTTTAATTCTTCTAAGAGTAAGTGAAGTGCAGTTG  
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT  
GTTTGGAAATATTATGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA  
TAGTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTGAAATA  
AAAATATTATATAAAAGTAAAAAAAAAA

## FIGURE 60

MVGAMWKIVSLVLLMPGCDGLFRSLYRSVSMPKGDSQPLFLTPYIEAGKIQKGREL  
VGPFPGNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTSNMTLRDRDFPWTTLSMLYIDNPVGTGSFTDDTHGYAVNEDDVARDLYSALIQF  
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFFEILDKLLDGLTSDPSYFQNV  
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNTFNDGTIVEKYLREDTVQSVKPWLT  
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEEKVWKIFKSDSEVAGYIRO  
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

**Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

**Tyrosine kinase phosphorylation site.**

amino acids 423-432

**N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

**Serine carboxypeptidases, serine active site.**

amino acids 200-208

**Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

## FIGURE 61

CGAGGGCTTCGGCTCCGAATGGCACATGTGGGAATCCCAGTCTGTTGGCTACAACAT  
TTTCCCTTCTAACAAAGTCTAACAGCTGTTAACAGCTAGTGATCAGGGGTTCTTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG  
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG  
TCTAAAATAGGAAGGAATTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGAGGGCCTGCCTAACAAAGCTTCAAAAAACAGGAGCAGTCCACTGGCTGGGAT  
AAGACGTGCCGGTAGGATAGGAAAGACTGGTTAGTCCTAACATATCAAATTGACTGGCTGGG  
TGAACCTAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTAACGGGCCAGAAA  
TAGAGATGCTTGTAAAATAAATTTAAAAAAGCAAGTATTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGAGGAGAAAGTATGTTAAAATA  
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAACACCAGGATGGGACCTGGGTC  
AGGCCAGCCTCTTGCTCCTCCGGAAATTATTTGGTCTGACCACTCTGCCTTGTGTTT  
GCAGAATCATGTGAGGGCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT  
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGCCCTGGAGGTGG  
ACAGCCGCTCTGTGGCCTGCTCTCAGTGGCTGGGTGCTGCTGGCCCCCCCAGCAGCCGGC  
ATGCCTCAGTTCAGCACCTTCACTCTGAGAAATCGTGAUTGGACCTTCAACCACCTGACCGT  
CCACCAAGGGACGGGGCGTCTATGTGGGGCATCAACCGGGTCTATAAGCTGACAGGCA  
ACCTGACCATCCAGGTGGCTATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTACCCG  
CCCTCATCGTGAGCCCTGCAGCGAAGTGCTCACCTCACCAACATGTCAACAAAGCTGCT  
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGAGCCTCTACCAGGGGTCTGCA  
AGCTGCTGCCGCTGGATGACCTCTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC  
CTGTCAGTGTCAACAAGACGGGCACCATGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA  
TGGCAAGCTCTTCATGGCACGGCTGTGGATGGAAAGCAGGATTACTTCCGACCTGTCCA  
GCCGGAAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGAT  
TTTGTCTCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCCACTTGACAT  
CTTCTACATCTACGGCTTGTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCGAGA  
CCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTACACCTCACGCATCGTCCGG  
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGTCCTGCCCTGGCTGCACCCGGC  
CGGGGTGGAATACCGCCTCTGCAGGCTGCTTACCTGCCAACGCTGGGACTCACTGGCCC  
AGGCCTCAATATCACCAAGCCAGGACGATGTACTCTTGCCATCTCTCAAAGGGCAGAAG  
CAGTATCACCAACCGCCCGATGACTCTGCCCTGTGCTCCCTATCCGGGCATCAACTT  
GCAGATCAAGGAGCGCCTGCAGTCTGCTACCAAGGGCAGGGCACCTGGAGCTCAACTGGC  
TGCTGGGAAGGACGCCAGTGCACGAAGGCGCTGTCCCCATCGATGATAACTCTGTGGA  
CTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTGTACACCAC  
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTG  
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCC  
ATTCACCTCTCAGCAAAGAGTCCCTCTGGAAAGGTAGCTATTGGTGGAGATTTAACTATAG  
GCAACTTATTTCTGGGAACAAAGGTGAAATGGGGAGGTAAGAAGGGTTAATTTGTG  
ACTTAGCTCTAGCTACTCCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA  
TTCAATATTCCTAAACTTTAAGAAAAACTTTAAGAAGGTACATCTGCAAAAGCAAA

## FIGURE 62

MGTLGQASLFAPPNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP  
RALEVDSRSVVLSSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV  
YKLGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLLACGSL  
YQGVCKLLRLDDLFLILVEPSHKKEHYLSSVNKTGTMGVIVRSEGEDGKLFIGTAVDGKQDY  
FPTLSSRKLPKDPESSAMLDYELHSDFVSSLIKIPIPSDTLALVSHFDIFYIYGFASGGFVYFL  
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSLQAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEGN  
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG  
YSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKESSLLEGSYWWRFNYRQLYFLGEQR

**Signal sequence:**

amino acids 1-32

**Transmembrane domain:**

amino acids 71-87

**N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

**Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## **FIGURE 63**

AGGCTCCCGCGCGCGGCTGAGTGGACTGGAGTGGAAACCGGGTCCCCCGCCTTAGAGAACACCGCGATGACCA  
CGTGGAGCCTCCGGCGGAGGCCGGCCCGCACCGCTGGACTCTGCTGCTGGTCCTGGGCTTCCTGGTGCCTCC  
GCAGGCTGGACTGGAGCACCCCTGGTCCCTCTGCGGCTCCGCATCGACAGCTGGGCTGCAGGCCAAGGGCTGGA  
ACTTCATGCTGGAGGATTCCACCTTCTGGATCTCGGGGCTCCATCCACTATTTCCGTGTGCCAGGGACTACT  
GGAGGGACCGCTGCTGAAGATGAAGGCCTGGCTTGAAACACCCCTCACCACTATGTTCCGTGGAACCTGCATG  
AGCCAGAAAGAGGCAAATTGACTTCTCTGGGAACCTGGACCTGGAGGCCCTCGCCTGATGGCCAGAGATCG  
GGCTGTGGGTGATTCTGCGTCCAGGCCCTACATCTGCACTGAGATGGACCTGGGGCTTGCCAGCTGGCTAC  
TCCAAGACCTGGCATGAGGCTGAGGACAACCTACAAGGGCTCACCGAAGCAGTGGACCTTATTGACCAC  
TGATGCCAGGGTGGTGCACCTCCAGTACAAGCGTGGGGACCTATCATTGCCGTGCAGGTGGAGAATGAATATG  
GTTCTATAATAAAAGACCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGCCGTCATTGTGGAACCTGC  
TCCTGACTTCAGACAACAAAGGATGGCTGAGGAGGGATTGTCCAGGGACTCTGGCCACCATCAACTTGCACT  
CAACACACGAGCTGCAGCTACTGACCACCTTCTCTCAACGTCAGGGACTCAGGCCAAGATGGTATGGAGT  
ACTGGACGGGGTGGTTGACTCGTGGGAGGCCCTCACAAATCTGGATTCTCTGAGGGTTTGAACACCGTGT  
CTGCCATTGTGGACGCCGCTCCATCAACCTCTACATGTTCCAGGGACCAACTTGGCTCATGAATG  
GAGCCATGCACCTCCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTGCTGACAGAACGCCGCG  
ATTACACGGCCAAGTACATGAAGCTCGAGACTTCTGGCTCCATCTCAGGCATCCCTCCCTCCCCCACCTG  
ACCTCTTCCCAAGATGCCGTATGAGCCCTAACGCCAGTCTGTACCTGTCCTGTGGGACGCCCTCAAGTACC  
TGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCT  
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCACGTGCATGATGGGGCAGG  
TGTGTTGAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT  
ACACCGTGTGAGGATCTGGTGGAGAATCGTGGGAGCTCAACTATGGGAGAATATTGATGACCAAGCGCAAAG  
GCTTAATTGAAATCTCTATCTGAATGATTCAACCCCTGAAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA  
GCTTCTTCAGAGGTTGCCCTGGACAAATGGNGTTCCCTCCAGAAACACCCACATTACCTGCTTCTTCTGG  
GTAGCTTGTCCATCAGCTCCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGAGAAGGGGGTTGTATTCA  
TCAATGCCAGAACCTTGACGTTACTGGAACATTGGACCCCAGAAGACGCTTACCTCCAGGTCCCTGGTTGA  
GCAGCGGAATCAACCAGGTACCGTTTGAGGAGACGATGGGGCCCTGCATTACAGTCACGGAACCCCCC  
ACCTGGCAGGAACCAGTACATTAAGTGAGCGGTGGCACCCCTCTGCTGGTGCCTGGGAGACTGCCGCTC  
CTCTTGACACTGAAGCCTGGCTGCTGCCACCCCTCACTGCAAAAGCATCTCTTAAGTAGCAACCTCAGGG  
ACTGGGGCTACAGTCTGCCCTGTCAGCTCAAACCCCTAAGCTGCAGGGAAAGGTGGATGGCTCTGGGCC  
TGGCTTGTGATGATGGCTTCTACAGGCCCTGCTTGTGCCAGGCTGTCGGCTGTCTAGGGTGGAGC  
AGCTAATCAGATGCCACGCCCTTGCCCTCAGAAAAAGTGTGAAACCGTGCCTTGCCACGGACGTACAGCCC  
TGCAGCATCTGCTGGACTCAGCGTGCTTGTGCTGGTCTGGGAGGCTGGCACATCCCTCATGGCCCCAT  
TTTATCCCCGAAATCCTGGGTGTGTCACCAGTGTAGAGGGTGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT  
CTTCCCTCACACCTCTGAGCCTTCTGGGATTCTGGAAGGAACCTGGCGTGAAGAACATGTGACTTCCCCCTT  
TCCCTCCCACTCGCTGCTTCCACAGGGTGACAGGCTGGGCTGGAGAACAGAAATCTCACCCCTGCGTCTTCC  
CAAGTTAGCAGGTGCTCTGGTGTTCAGTGAGGAGGACATGTGAGTCCTGGCAGAACGCCATGGCCCATGTCTGCA  
CATCCAGGGAGGAGGACAGAACGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCCATGTCTGCAACATCC  
AGGGAGGAGGACAGAACGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCCATGTCTGCAACATCCAGGG  
GGAGGACAGAACGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCCATGTCTGCAACATCCAGGGAGGAGG  
ACAGAACGCCAGCTCAGTGGCCCCGCTCCCCACCCCCCAGGCCAACAGCAGGGGAGGAGCACGCCCTCCTC  
GAAGTGTGTCCAAGTCCGATTGAGCCTGTTCTGGGGCCAGCCAAACACCTGGCTTGGCTACTGCTCTGA  
GTTGCAGTAAAGCTATAACCTGAATCACAA

## FIGURE 64

MTTWSLRRR PARTL GLLL VVLGFLV LRR LDWSTLVPL RL RHRQL GLQAK GWN FM LED STFW  
I FGGS I HYF RV PREY WR DR LL K MKAC GL NT LTT Y VP WNL HEP ERG K F D FSG NLD LEAF VL MA  
AEI GLW VIL R PGP YIC S E M DL GGL P SW LL QD P GM RL RT TY KGF TEA VD LY FD HLM SRV VPL Q  
Y KRGG PI I AV Q VEN EY GS Y NK DP AY MP YV KKA EDRG I VELL L TSDN K DGL SKG I V QGV LAT  
IN LQ S T H E L Q L L T F L F NV Q GT Q PKM VM EY WT GWF D SW GG PHN I L DS SEV L KTV SAI VD AGS  
S IN LY MF HG GT NF GFM NGAM HF HDY K SD V TS Y DY D A V L T E A G D Y T A K Y M K L R D F F G S I S G I P  
L PPP P D L L P K M P Y E P L T P V L Y L S L W D A L K Y L G E P I K S E K P I N M E N L P V N G G N G Q S F G Y I L Y E  
T S I T S S G I L S G H V H D R G Q V F V N T V S I G F L D Y K T T K I A V P L I Q G Y T V L R I L V E N R G R V N Y G E N  
I DD Q R K G L I G N L Y L N D S P L K N F R I Y S L D M K K S F F Q R F G L D K W X S L P E T P T L P A F F L G S L S I S  
S T P C D T F L K L E G W E K G V V F I N G Q N L G R Y W N I G P Q K T L Y L P G P W L S S G I N Q V I V F E E T M A G P A  
L Q F T E T P H L G R N Q Y I K

**Signal sequence:**

amino acids 1-27

**Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

**N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

## **FIGURE 65**

GGGGACGCGGAGCTGAGAGGGCTCCGGCTAGCTAGGTAGGGGTGGACGGTCCCAGGACC  
CTGGTGAGGGTTCTACTTGGCCTTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG  
GGAGCAAAGCCGGCTCGGCCGAGGCCCCCAGGACCTCCATCTCCAATGTTGGAGGAATC  
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC  
AAGAAGCTGCTCGCTTCGTTCTGCTGAGTGGATAGGGTCATGACCGGTTCTCCTAGACGGGGCC  
GGCAGACACTCGGTGTTCTGAGTGGATAGGGTCATGACCGGTTCTCCTAGACGGGGCC  
CGTCCGCTATGTGCTGGCAGCCTGCACTACTTCGGTACCGCGGGTGCCTTGGGCCGAC  
CGGCTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTATGTGCCCTGGAACTA  
CCACGAGCCACAGCCTGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCCTTCTGA  
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG  
TGGGAGATGGGGGTCTCCCATCCTGGTCTCGAAAACCTGAAATTCTATCTAAGAACCTC  
AGATCCAGACTTCCTGCCGAGTGGACTCCTGGTTCAAGGTCTGCTGCCAAGATATATC  
CATGGCTTATCACAAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC  
TACAGAGCCTGTGACTCAGCTACATGAGGCACTTGGTCTGGCTCTCGTGCAGTGCAG  
AGAAAAGATCTGCTCTCACACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG  
GAECTATACCACTGTAGATTGGCCCAGCTGACAACATGACCAAAATCTTACCCCTGCTT  
CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA  
CTGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC  
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG  
AATGGTGCCATAAGAAGGGACGCTCCTCCGATTACTACCAGCTATGACTATGATGCACC  
TATATCTGAAGCAGGGACCCCACACCTAACGCTTTTGCTCTCGAGATGTCATCAGCAAGT  
TCCAGGAAGTTCCCTGGGACCTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG  
ACTCTGCACCTGGTGGCATTACTGGCTTCTAGACTTGCTTGGCCCGTGGGCCCAT  
TCATTCAATCTGCCATGACCTTGGAGGCTGTCAAGCAGGACCATGGCTCATGTTGTACC  
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGTGCCAAATAATGGAGTC  
CATGACCGTGCCTATGTGATGGTGGATGGGTGTTCCAGGGTGTGGAGCAGAACATGG  
AGACAAACTATTTTGACGGGAAACTGGGTCCAAACTGGATATCTGGTGGAGAACATGG  
GGAGGCTCAGCTTGGGCTAACAGCAGTGAACAGCAGGCTGGAGGCAACCAATTCTG  
GGCAAACAACTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG  
GTGGTTCCCTCCAGTTGCCAAATGCCATATCCTCAAGCTCTTCTGGCCCCACATTCT  
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG  
ACCAAGGGCCAAGTCTGGATCAATGGTTAACCTGGGCCGTACTGGACAAAGCAGGGCC  
ACAACAGACCCCTCACGTGCCAAGATTCTGCTGTTCTAGGGAGCCCTAACAAAATA  
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC  
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG  
TGCCTCTGAACCAATGGAGTTAAGTGGCACTGAAAGGTAGGCCGGCATGGTGGCTCATGC  
CTGTAATCCCAGCACCTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA  
CCAGCCTGGCCAACATGGTAAACCCCGTCTCCACTAAAAATAACAAAATTAGCCGGCGTG  
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTGAATCC  
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA  
GACACTCCATCTCAAAAAAAAAAA

## **FIGURE 66**

MAPKKLSCLRSLLLPLSLTLLPQADTRSFVVDRGHDFLLDGAPFRYVGSLHYFRVPRVL  
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVE  
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF  
TLLRKYEPHGPLVNSEYYTGWLWQNHSTRSAVTKGLENMLKLGASVNMYMFHGGTNF  
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPGLPPPSPKML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTFWVPN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRSLFGSNSSDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL  
PGWTKGQVWINGFNLGRYWTQOGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

**Signal sequence:**

amino acids 1-27

**N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

**Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

**Tyrosine kinase phosphorylation site.**

amino acids 191-198

**N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## FIGURE 67

GCTTGAAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTGAGTGC  
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT  
TTATGGCTTATCTGCCTCTACACTCTTCTGGTTATTCAAGGATACTTGAAGGAATATT  
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGCACATTCCAGATGTCAAAAACGATTT  
GCGTTCCCTTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT  
CTTGTCAAGTTAGTGAACCTAGGGAAATTAGTTGAACCATGAGTGGACATTG  
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG  
CTGTCGGGGGTGCCGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC  
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTTGAGA  
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCCTGCCTGGGTGTATTGCTCAAAAA  
CCTTCGAGAGTTGTACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGCCGACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTAACAAAGTTAGTCATTATAATGACGGCAC  
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA  
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACAGGAACGGAT  
TTAAAGTCCAATAACATTGCACAATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT  
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTTATTACCCATGTCA  
AAAACTTGGAGTCACTTATTCTCTAACACAACAGCTGAATCCTTACCAAGTGGCAGTATT  
AGTTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAAACATTCAATGATTCCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC  
CAAAACAATTGTTAAATGCATAAAAGTTGAGGACTTTGAATCTGGACAGAACTGCATCACC  
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCAGCTGGAGCTGAAGGGAACTG  
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGTTGTG  
TGGAAGATCACCTTTGATAACCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA  
AATATTCCCTTGCAAATGGATTTAACTAAGATAATATATGCACAGTGTGAGTGCAGGAAC  
AACTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG  
ATACATCTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTGAGGGTTTAAGTCATTCAACATTCAAGTAAATTGTTTTCTTTGGGG  
AAAGGGAAGGAAAATTATAATCACTAATCTGGTTCTTTAAATTGTTGTAACCTGGAT  
GCTGCCGCTACTGAATGTTACAAATTGCTGCCTGCTAAAGTAAATGATTAAATTGACATT  
TTCTTACTAAAAAAAAAAAAAA

## FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL  
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLQRQHISRNAQDKQELHLFMLSG  
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMNTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH  
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLESLRELRLKILHVKSNLTKVPSN  
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCELERIPHAIIFSLSNLQELDLKS  
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTISSITHVKNLESLYFSNNKLESLPVAVFSLQ  
KLRCLDVSYNNISMPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP  
EKVGQLSQLTQLELKGNCNDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP  
FANGI

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

**Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

**Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

**N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

## FIGURE 69

CCACACGCGTCCGGCCTCTCTGGACTTTGCATTCCATTCCCTTTCATGACAAACTGACTTTTTATTC  
TTTTTCCATCTCTGGGCCAGCTGGGATCCTAGGCCGCCGGAAAGACATTGTGTTTACACACATAAGGAT  
CTGTGTTGGGTTCTTCTCCTCCCCTGACATTGGCATTGCTTAGTGGTGTGTTGGGAGGGAGACCACGTGG  
GCTCAGTGCTTGCTGCACTTATCTGCCTAGGTACATCGAAGTCTTGACCTCCACAGTATTATGCCTGTC  
ATCGCTGGTGTATCCTGGCGCTGCTCTGCTGATAGTTGTCGTCTGTCTTACTTCAAACACAAAC  
GCGCTAAAAGCTGCAAAGAACCTGAAGCTGTCGTGAAAAACACAACCCAGACAAGGTGTGGTGGCCAAG  
AACAGCCAGGCCAAAACCATTGCCACCGAGCTTGTCCCTGCCCTGCAGTGTGAGGATATAGAATGTGTGCC  
AGTTTGATTCCCTGCCACCTTGCGACATAAATGAGGGCTCTGAGTTAGGAAAGGCTCCCTCTCAAAC  
GCAGAGCCCTGAAGACTTCAATGATGTCATGAGGCCACCTGTTGTGATGTGCAGGCACAGAAGAAAGGCACAG  
CTCCCCATCAGTTCATGAAAATAACTCAGTGCTGCTGGGAAACAGCTGCTGGAGATCCCTACAGAGAGCTTC  
CACTGGGGGCAACCTTCCAGGAAGGAGTTGGGGAGAGAGAACCCCTACTGTGGGAATGCTGATAAAACCAAGTCA  
CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCTGAACTGACGTTCCCTGGAGGTGTCCAGAAA  
GCTGATGTAACACAGAGCTATAAAAGCTGTCGGCTTAAGGCTGCCAGGCCCTGCCAAAATGGAGCTTGT  
AGAAGGCTCATGCCATTGACCTCTTAATTCTCTGTTGGCGAGCTGACAATGGGGAGGCTGAAGGCAAT  
GCAAGCTGCACAGTCAGTCTAGGGGTGCAAATATGGCAGAGACCCACAAAGCCATGATCTGCAACTCAATCCC  
AGTGAGAACTGCACCTGGACAATAGAAAAGACAGAAAACAAAGCATCAGAATTATCTTCTATGTCCAGCTT  
GATCCAGATGGAAGCTGTGAAAGTGAACATTAAGTCTTGACGGAACCTCCAGCAATGGCCTCTGCTAGGG  
CAAGTCTGCAGTAAAAGACTATGTCCTGATTGAAATCATCAGTACATTGACGTTCAAATAGTTACT  
GACTCAGCAAGAATTCAAAGAACTGTCCTTGTCTTACTACTTCTCTCTCCTAAACATCTCTATTCCAAACTGT  
GGCGGTTACCTGGATACCTTGGAGGATCCTCACAGGCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT  
TGTGTTGGCACATACAAGTGGAGAAAAGATTACAAGATAAAACTAACTCAAAGAGATTTCCTAGAAAATAGAC  
AAACAGTGCACATTGATTCTGCCATCTATGATGGCCCTCCACCAACTCTGGCTGATTGGACAAGTCTGT  
GGCCGTGTGACTCCCACCTCGAACATCGTCATCAAACCTCTGACTGTCGTGTTGCTACAGATTATGCCAATTCT  
TACCGGGATTCTGCTTCTACACCTCAATTATGCAAGAAAACATCAACACTACATCTTAACTTGTCTTCT  
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGTTTAACTCTAATGGGAAATACTTGCACACTAAA  
GACCCAACTTGCAGACCAAATTATCAAATGTTGGAATTCTGCTCCCTTAATGGATGTGGTACAATCAGA  
AAGGTTAGAAGATCAGTCACATTACACCAATATAATCACCTTCTGACTCCTCAACTCTGAAGTGTACCC  
CGTCAGAAACAACTCCAGATTATGTAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATAACATAACA  
GAAGATGATGTAATAACAAAGTCAAATGCACTGGGAAATATAACACCCAGCATGGCTTTGAATCCAATTCA  
TTGAAAAGACTATACTTGAATCACCATATTATGTTGGAATTGAAACCAACTCTTGTCAAGTTAGTCTGCAC  
ACCTCAGATCCAAATTGTTGTTCTGATACCTGACTGAGATGAAACTTGTAAAGGTGTATCCCTATTGGACACTATGGGAGA  
TTCCAGTTAATGCCCTTAAATTCTGAGAAGTATGAGCTGTGTTCTGCACTGTAAGTTGATATGTGAT  
AGCAGTGGACCAACCAGTCTGCTGCAATCAAGGTTGTCCTCCAGAAGCAACCGAGACATTCTCATATAATGG  
AAAACAGATTCCATCATAGGACCCATTGCTGAAAAGGGATGCAAGTGCAAGTGGCAATTCAAGGATTTCAGCAT  
GAAACACATGCCAGAAAACCTCAAACCCAGCCTTCAACAGTGTGCATCTGTTCTCATGGTTCTAGCTCTG  
AATGTGGTACTGTAGCGACAATCACAGTGAGGCTTTGAAATCAACGGGAGACTACAAACACAGAAGCTG  
CAGAACTATTAACTAACAGGTCCAACCTAAGTGAGACATGTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT  
GGCTACACATATTGAATAATGAGGAAGGGCTGAAAGTGACACACAGGCCCTGCATGAAAAAAA

## **FIGURE 70**

MELVRRLMPLTLIILSCLAEALTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIRIIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLGVCSKNDYVPVFESSSSTLT  
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCRVTPTFESSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP  
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIIITFSASSTSEVITRQKQLQIIVKCEMGNST  
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN  
LVVFLDTCRASPTDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNFKFLRSMSSVYL  
QCKVLICDSSDHQSRCNQGCVRSRKDISSYWKTDIIGPIRLKRDRSASGNSGFQHETHA  
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

**Signal sequence:**

amino acids 1-24

**Transmembrane domain:**

amino acids 571-586

**N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

**Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

**N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 71**

GACGGAAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCTGCGCCG  
GGACATGCGGCCCCAGGAGCTCCCAGGCTCGCGTCTCGCTGCTGTGCTGCTGC  
TGCTGCCGCCGCCGTGCCCTGCCACAGCGCCACGCCAGGGCAAGTCGGCATCTCATCCACTG  
CTGGACGCCGCCAGCTGCCCGTGGTTGACCAGGCCAAGTCGGCATCTCATCCACTG  
GGGAGTGTTCCTCGCCAGCTCGTAGCGAGTGGTCTGGGGTATTGGAAAAGGAAA  
AGATACCGAAGTATGTGAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT  
TTGGACCACTATTACAGCAAATTAAAAATGCAACAGTGGCAGATATTTCAGGC  
CTCTGGTGCAAATACATTGTCTTAACCTCAAACATCATGAAGGCTTACCTTGTTGGGGT  
CAGAATATTGTGGAACTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA  
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCCTGGACTGTACTATTCCCTTTGA  
ATGGTTTCATCCGCTTCCTGAGGATGAATCCAGTCATTCCATAAGCGGAATTTCAG  
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATCAGCCTGAGGTCTGTGG  
TCGGATGGTACGGAGGGCACCGGATCAAACTGGAACAGCACAGGCTCTTGGCCTGGTT  
ATATAATGAAAGCCCAGTCGGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA  
TCTGTAAGCATGGTGGCTTCTACCTGCAGTGATCGTTATAACCCAGGACATCTTGCCA  
CATAAATGGAAAAGTCATGACAATAGACAAACTGTCCTGGGCTATAGGAGGAAGCTGG  
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTCATGTG  
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTCTGTAGTTTGAG  
GAGCGACTGAGGCAAGTGGGCTGGCTAAAGTCATGGAGAGCTATTATGAAACCTA  
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATTCTAAATGGGCCACATCAGGACAGCTGTTCTGGCCAT  
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGCCATGGACAGCCACTTAAC  
GATTCTTGAGCAAATGGCATTATGGTAGAACTGCCACAGCTAACCAATTGATGC  
CGTGTAAATGGGCTGGCTAGCCCTAACTATGTGATCTAAAGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA  
AAGCAATGTAACGGATAAGAAAATTATGGCAGTTCCAGGCCCTTCCCTTCCCCTA  
AATTCTAAATTACCCATGTAACCATTAACTCTCCAGTGCACCTTGCCATTAAAGTC  
TCTTCACATTGATTGTTCCATGTGTGACTCAGAGGTGAGAATTTCACATTATAGTAG  
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTATGTTGAAGCCATATCCCCCATG  
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAT  
TTTTTTGTGCCAACATCATAGAGTGTATTACAAAATCTAGATGGCATAGCTACTACA  
CACCTAATGTGTATGGTATAGACTGTCCTAGGCTACAGACATATACAGCATGTTACTG  
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG  
GTACAGTAAAATACTGTAAAATGGTGCACCTGTATAGGGCACTTACCCAGGAATGGAG  
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA  
TTGAACACTGCCAGACGTTATAAAACTGTATGCTTAGGCTACACTACATTATAAAAAAAA  
GTTTTCTTCTTCATTATAAACATAAGTGTACTGTAACTTACAAACGTTTAATT  
TTTAAACCTTTGGCTTTGTAATAACACTTAGCTAAACATAAAACTCATTGTGCAA  
ATGTAA

## FIGURE 72

MRPQELPRLAFPLLLLLLPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHG  
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTA  
KFFNANQWADIFQAS  
GAKYIVLTSKHHEGFTLWGSEYSWNNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLFEW  
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNTQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVVRGTVVTNDRGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETY  
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHQPLNW  
SLEQNNGIMVELPQLTIHQMPCKWGWALALTNVI

**Signal sequence:**

amino acids 1-28

**N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

**Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

**Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

**N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

**Leucine zipper pattern.**

amino acids 410-432

**Alpha-L-fucosidase putative active site.**

amino acids 283-295

## FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT  
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGCCATC  
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGCCAGGTGCTTCAGCCTGGTGTG  
CTTCTCACTCCATCTGGACCACGAGGCTCTGGCCAAGGCTTTGCGTGAGAAGAGCT  
TTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCCCTGTGAGCAAAAGGCGAACCGC  
AGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCCGGCAAG  
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAACATTCAGCTATGGCTGGGTGGAGA  
TGGATTCGTGGTCATCTCTAGGATTAGCCCCAACCCCAAGTGTGGAAAAATGGGGTGGGTG  
TCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTGCAGCTATTGTTACAACTCATCTGAT  
ACTTGGACTAACCTGTCATTCCAGAAATTATCACCACCAAAGATCCCATAATTCAACACTCA  
AACTGCAACACAAACAAACAGAATTATTGTCACTGACAGTACCTACTCGGTGGCATCCCCCT  
ACTCTACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTCCACTTCTATTCCACGG  
AGAAAAAAATTGATTTGTGTCACAGAAGTTTATGAAAACAGCACCATGTCTACAGAAAC  
TGAACCATTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC  
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGAGCTGGCTTGGATTTC  
TATGTCAAAAGGTATGTGAAGGCCTCCCTTACAAACAAGAATCAGCAGAAGGAAATGAT  
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAATGAGGAATCAAAGA  
AAACTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGCATGCCCTGGAA  
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC  
TTACCCCTGCCCTAGCTGGGAAATCAAAGGCCAAAGAACCAAAGAAGAAAGTCCACCCTT  
GGTTCTTAACGGAAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC  
CCTTCTCCTTATTGTAACCCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC  
TTTCTAGCCTGGCTATGTCCTAATAATATCCCACGGAGAAAGGAGTTTGCAAAGTGCAA  
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTGAGGCTAGG  
TGGGTTGAAAGCCAAGGAGTCAGTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGAC  
CCTTCTCAGCTCTGAAAGAGAACACGTATCCCACCTGACATGTCCTCTGAGCCCGGTA  
AGAGCAAAAGAATGGCAGAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG  
ACCTAATCTCTGAAAGCTAAAATAAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACT  
GTCAGCAGGGACTGTAACACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGA  
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTTCT  
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAATTCTATTTTATCTGA  
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA  
ACAAACATTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT  
TGAATATTATCCTCAAAAATTGCACATAGTAGAACCGCTATCTGGGAAGCTATTTTCA  
GTTTGATATTCTAGCTTATCTACTTCCAAACTAATTGTTATTGCTGAGACTAATCTT  
ATTCAATTCTCTAATATGGCAACCATTATAACCTTAATTATTAAACATACCTAACAG  
TACATTGTTACCTCTATATACCAAAGCACATTAAAAGGCCATTAACAAATGTATCACTA  
GCCCTCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAATTAA  
AGCATTAGAAAACCTT

## FIGURE 74

MARCFSLVLLLTSIWTTRLLVQ GSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR  
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISP NPKCGKNGVGVLIW KVPVSRQF  
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKA AAFKNEAAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKA FPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP  
SKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## **FIGURE 75**

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTATTGGTGCACGACTTCACGATGG  
CTGGCCAACCTTACTACCTCTGTCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA  
ACTGCCGCCCTGCCACGGCTGCCACCCAACGCGAAGACGGTAACCGTGTGACTTTG  
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCATTGTGATGATGAAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAAACACAAT  
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC  
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGAACTAGAACGGACAAGAGGGTCACTGGATTGTGGAGTTCTTGCAA  
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC  
GTACAGGGCTAAATTGGGAAGGTGGATGTTGGACGCTACTGATGTTAGTACGGTAC  
AAAGTGAGCACATCACCCTCACCAAGCAACTCCCTACCCCTGATCCTGTTCCAAGGTGGCAA  
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTCTCG  
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGCCAAGAAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACCACAGTGTCA  
TGGGAAAACAAGAAGGATAAATAAGATCCTCACTTGGCAGTGCTCCTCTCCTGTCAATT  
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTCCCTTGG  
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTAAAGAGGCATCTAGGAATTGTCAG  
GCACCCTACAGGAAGGCCTGCCATGCTGTGCCACTGTTCACTGGAGCAAGAAAGAGATC  
TCATAGGACGGAGGGGGAAATGGTTCCCTCCAAGCTGGTCAGTGTGTTACTGCTTATC  
AGCTATTAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCCCTTAG  
TTGACCTGCACAGCTGGTTAGACCTAGATTAAACCTAACGTAAGATGCTGGGTATAGAA  
CGCTAAGAATTTCACCAAGGACTCTGCTTCTTAAGCCCTCTGGCTCGTTATGGTC  
TTCATTAAAGTATAAGCCTAACCTGTCGCTAGTCCTAACGGAGAACCTTAACCACAAAG  
TTTTTATCATTGAAGACAATTGAACAACCCCCCTATTGTGGGATTGAGAAGGGGTGAA  
TAGAGGCTTGAGACTTCCTTGTGTGGTAGGACTTGGAGGAGAAATCCCTGGACTTCAC  
TAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT  
TCCTTTG

## **FIGURE 76**

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMF SKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC  
TGLNFKGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRACKLSKAGDNIPEEQPVASTPTVSDGENKKDK

**Signal sequence:**

amino acids 1-48

**Transmembrane domain:**

amino acids 111-125

**N-glycosylation site.**

amino acids 165-169, 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

**Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

**N-myristoylation site.**

amino acids 188-194, 225-231

**Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

## **FIGURE 77**

GGACAGCTCGGGCCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCCTGGGACGTTGCCCTG  
GGGCCCTGGCCGGTCACCCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCC  
TTGCTCCTGCTGCCGGCTCCTACGGACTGCCCTCTACAACGGCTTACTACTCCAACAG  
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG  
TGGTGGAGACACCCGAGGGAGACCCCTGTTACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC  
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGGCGTGTGCGTGTCAAATGGTGGAAAGCT  
GTCGGAGAACGGGCCAGAGAAGGACGTGCTGGTGGCCATGGGCTGAGGCACCGCTCCT  
TTGGGACTACCAAGGCCGCGTGCACCTGGCAGGACAAAGACCATGACGTCTCGCTGGAG  
ATCCAGGATCTCGGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTATTGACGGCTGGAA  
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTTCTTACCAAGTCCCCCA  
ACGGCGCTACCAAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCC  
GTGGCCTCCTTGAGCAGCTCTCCGGGCTGGAGGAGGGCTGGACTGGTGCACCGGG  
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCC  
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACGCCCTGCACCGCTATGAT  
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCCGTAGAAGCT  
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC  
AGCTTTGCCGCTGGAAGTTCACTGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT  
GGCAGCGTCCGCTACCCGTGGTTCACCCGATCCTAAGTGTGGCCCCAGAGCCTGGG  
CCGAAGCTTGCTTCCCCGACCCGAGAGCCGTTGTACGGTGTACTGCTACCGCCAGC  
ACTAGGACCTGGGCCCTCCCGCCATTCCCTGCGCATTCCCTACTGGCTGTATTATTGAGTGGTT  
CGTTTCCCTGTGGGTTGGAGCCATTAACTGTTTATACTTCTCAATTAAATTCT  
TTAACATTTTACTATTTTGAAAGCAAACAGAACCCATGCCCTCCCTTGCTCCTG  
GATGCCCACTCCAGGAATCATGCTTGCTCCCTGGCCATTGCGGTTGTGGCTTCTG  
GAGGGTCCCGCCATCCAGGCTGGCTCCCTCCCTTAAGGAGGTTGGGCCAGAGTGGC  
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGCATGGTGGCACAGTTCTCCCTGCC  
CAGCCTGGGGAAAGAAGAGGGCCTGGGGCTCCGGAGCTGGCTTGCGCTCTCCTGCC  
CACCTCTACTTCTGTGAAGCCGCTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA  
GCCAGTTCTAGGCTCAGGCGAAATCTGAGGGAAGGAAGAAACTCCCCCTCCCCGTTCC  
TCCCTCTCGGTTCAAAGAATCTGTTGTTGTCATTGTTCTCCTGTTCCCTGTGTGG  
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGCTATGACTGCCCTGGCAA  
AA  
AA

## **FIGURE 78**

MGLLLVPLLLPGSYGLPYNGFYYNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGP  
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

**Signal sequence:**

amino acids 1-17

**Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

**Tyrosine kinase phosphorylation site.**

amino acids 137-145

**N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

## **FIGURE 79**

GGAGAGCGGAGCGAAGCTGGATAACAGGGACCG**TG**GATGTGGCGACCATCAGTTCTGCTGC  
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC  
CAGGGGAGGGTGCACCAGGGCCCTGAGCGACGCTCCCCATGATGACGCCACGGAA  
CTTCCAGTACGACCATGAGGCTTCCTGGACGGAAAGTGGCAAGGAATTGACCAACTCA  
CCCCAGAGGAAAGCCAGGCCGTCTGGGCGGATCGTGGACCGCATGGACCGCGGGGGAC  
GGCGACGGCTGGGTGTCGCTGGCGAGCTCGCGCTGGATCGCGCACACGCAGCAGCGA  
CATACGGACTCGGTGAGCGCGCCTGGACACGTACGACACGGACCGCGACGGCGTGTGG  
GTTGGGAGGAGCTCGCAACGCCACCTATGCCACTACGCGCCGGTGAAGAATTGAC  
GTGGAGGATGCAGAGACCTACAAAAGATGCTGGCTCGGACGAGCGGGCTTCCGGTGGC  
CGACCAGGATGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTCCTGCACCCCGAGG  
AGTCCCTCACATGCGGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA  
GATGGCTATGTCCAGGTGGAGGAGTACATCGGGATCTGTACTCAGCCGAGCCTGGGAGGA  
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTCCGGACTTCCGGATCTGAACAAGG  
ATGGGCACCTGGATGGAGTGAGGTGGCCACTGGGTGCTGCCCTGCCAGGACCGAGCCC  
CTGGTGGAAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAA  
AGCGGAAATCCTGGTAATTGGAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG  
ACCTGACCCGGCACCAAGATGAGCT**TG**AGCACCAGCGCACCTGCCACAGCCTCAGAGGCCCG  
CACAAATGACCGGAGGAGGGCCGCTGTTCTGGCCCTCCCTGTCCAGGGCCCGAGGAG  
GCAGATGCAGTCCCAGGCATCCTCTGCCCTGGCTCTCAGGGACCCCTGGGTGGCTTC  
TGTCCCTGTACACCCCCAACCCAGGGAGGGCTGTCATAGTCCCAGAGGATAAGCAATAC  
CTATTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTGGCCCAAGCTCAGCTCTAA  
GAACCGCCCCAACCCCTCCAGCTCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCCT  
GGCCCCAGCCCTCTCTGCCTGGCCTGGACACCTCCTCTGCCAGGAGGAATAA  
AAGCCAGGCCGGACCTTGAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAA

## FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDWVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTDGRVGWEELRNATYGHYAPGEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE  
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ  
FRDFRDLNKDGHLDGSEVGHVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 140-144

**Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

**N-myristoylation site.**

amino acids 263-269, 311-317

**Endoplasmic reticulum targeting sequence.**

amino acids 325-330

## **FIGURE 81**

GGGGCCTTGCCTCCGCACTGGCGCAGCCGGTGGATCTGAGCAGGTGCGGAGCCCCGG  
GCGGCGGCGCGGGTGCAGGGATCCCTGACGCCTCTGCCCTGTTCTTGCTGCTCCCAG  
CCTGTCGTCGTTGGCGCCCCGCCTCCCGCGGTGCAGGGTTGCACACCGATCCTG  
GGCTTCGCTCGATTGCCGCCAGGCGCCTCCAGACCTAGAGGGCGCTGGCCTGGAGCAG  
CGGGTCGCTGTGTCCTCTCCCTCGGCCGCCGGGATCCGAAGGGTGCAGGGCTCT  
GAGGAGGTGACGCCGGGCTCCGCACCCCTGGCCTGCCGCATTCTCCCTCTCCAG  
GTGTGAGCAGCCTATCAGTCACCATTGTCGCAGCCTGGATCCCGCTCTGGCCTCGGTGTG  
TGTCTGCTGCTGCCGGGCCGCCAGCGAGGGAGCCGCTCCATTGCTATCACATG  
TTTACAGAGGCTTGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGCTGCC  
CTCTGAGGAATTCTCTGTATGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG  
GCTGCTGTCCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC  
TGGTCGAGAAAATATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT  
GGTCTGCTCTTCACAGTAACTAAAGGCAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAATGG  
CAATAAAGATTGTAAGCAGACATTGCATTCTGATTGATGGAAGCTTAATATTGGCAGC  
GCCGATTAATTACAGAAGAATTGTTGGAAAAGTGGCTCTAATGTTGGAAATTGGAACA  
GAAGGACCACATGTGGCCTTCAAGCCAGTGAACATCCAAAATAGAATTTACTTGAA  
AAACTTACATCAGCAAAGATGTTGTTGCCATAAGGAAGTAGGTTCAGAGGGGTA  
ATTCCAATACAGGAAAAGCCTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA  
GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTATTGATGGTGGCCTCTGATGACAT  
CGAGGAAGCAGGCATTGTGGCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCCA  
AGCCTATCCCTGAAGAACTGGGATGTTCAGGATGTCACATTGTTGACAAGGCTGCTGT  
CGGAATAATGGCTTCTCTTACACATGCCAATGGTTGGCACCACAAAATACGTAAA  
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT  
CAGTGAACATTGCCTTCTAATTGATGGCTCCAGCAGTGGAGATAGCAATTCCGCCTC  
ATGCTGAAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTCCAAGAT  
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCACTGACTATAGCACCA  
AAGAGAATGTCCTAGCTGTCACTCAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT  
GATGCCATTCTTCACTGTTAGAAATGTGTTGCCCTATAAGGGAGAGCCCCAACAGAA  
CTTCCTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCACAGGCCCTGCAGCTGCTG  
CACATGATGCAGGAATCACTATCTCTGTTGGTGTGGCTTGGCACCTCTGGATGACCTG  
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTCTTACAAGAGAGTTCACAGGATT  
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGTAGAGATTCTTACAATCCCAGCAAT  
**AATGGTAACATTGACAAC**TGAAAGAAAAAGTACAAGGGGATCCAGTGTGAAATTGTATT  
CTCATAATACTGAAATGCTTACTGATAGAATCAGATACAAAATATTAGTATGTCAAC  
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCCTGGTTACAATTACAGTGT  
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTTCAAGAAACTCAGGAAAGAGGA  
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA  
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAA

## FIGURE 82

MSAAWIPALGLVCLLLLPGPAGSEAAPIAITCFTRGLDIRKEKADVLCPGGCPLLEFSVY  
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDKADIAFLIDGSFNIGQRRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRGGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI  
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLA  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDQSYDDVQGPAAAHDAGITI  
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

**Signal sequence:**

amino acids 1-24

**N-glycosylation site.**

amino acids 100-104, 221-225

**Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

**N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

**Amidation site.**

amino acids 145-149

## **FIGURE 83**

CGCCCGCGCTCCCGCACCGCGGCCGCCACCGCGCCGCTCCGCATCTGCACCCGCAGCCC  
GGCGGCCTCCGGCGGGAGCGAGCAGATCCAGTCCGGGCCGCAGCGCAACTCGGTCCAGTCG  
GGGCGCGGCTGCGGGCGCAGAGCGGAGATGCAGCGGCTGGGCCACCCCTGCTGTGCCTGC  
TGCTGGCGGGCGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTC  
AAGCCCGGCCGGCTCTCAGCTACCCGAGGAGGACACGCAGCACAAATTGCGCAGCGGGTGAAGAGATGGAGG  
GGTGAGGAAGTGTGGAGGACACGCAGCACAAATTGCGCAGCGGGTGAAGAGATGGAGG  
CAGAAGAACGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACACTACCTCCCAGCTAT  
ACAATGAGACCAACACAGACACGAAGGTTGAAATAATACCATCCATGTGCACCGAGAAAT  
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG  
TGGGAGACGAAGAACGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC  
ATGTAAGTGCAGTTGCCAGCTCCAGTACACCTGCCAGCCATGCCGGGCCAGAGGATGCT  
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCAGCTGTGTCTGGGTCACTGCACCAAAA  
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG  
TGCTGTGCCTCCAGAGAGGGCTGCTGTTCCCTGTGTGCACACCCCTGCCGTGGAGGGCGA  
GCTTGCCATGACCCGCCAGCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG  
GAGCCTTGGACCGATGCCCTTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG  
GTGTATGTGTGCAAGCCACCTCGTGGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC  
CAGAGAGGTCCCCGATGAGTATGAAGTTGCCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG  
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGTGCCGCGCT  
GCACTGCTGGAGGGAAAGAGATT**TAGATCTGGACCAGGCTGTGGTAGATGTGCAATAGAA**  
ATAGCTAATTATTCCCCAGGTGTGCTTAGGCGTGGCTGACCAGGCTTCTTACA  
TCTTCTTCCCAGTAAGTTCCCCTCTGGCTTGACAGCATGAGGTGTTGCAATTGTTCA  
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGCTTGGAGAGTCAGGCAGGGTTAAC  
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTTACCAAGTTGGCAG  
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGGAGGAGATGGAAACAATGTGG  
AGTCTCCCTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAAACATCAA  
CCTGGCAAAATGCAACAAATGAATTTCACCGCAGTTCTTCCATGGGCTAGGTAAGCTG  
TGCCTTCAGCTGTTGAGATGAAATGTTCTGTCACCCGCATTACATGTGTTATTCA  
AGCAGTGTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT  
CCTCTCTCAGCACAGCCTGGGGAGGGGTCAATTGTTCTCCTCGCCATCAGGGATCTCAGAG  
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACAGAGCAGTTCAT  
CTGGTTGTGACTCTAACGCTCAGTGTCTCTCCACTACCCACACCAGCCTTGGTGCCACCAA  
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTTTCTTGAGGCATGCACATCTGAAATTAG  
GTCAAACATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC  
AGTGTGGGGCAGCGTCCCTCTAATGAAGACAATGATATTGACACTGTCCTCTTGGCAGT  
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATAACAGGTTAACCTGCAGAAACA  
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTGCAAACATTCACTTAGCAGCAAC  
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT  
GTAATTATGCGACTGCGAACACTGAACCTACGCCACTCCACAAATGATGTTTCAAGGTGTC  
TGGACTGTTGCCACCATGTATTGATCCAGAGTTCTTAAAGTTAAAGTTGACATGATTGTA  
TAAGCATGTTCTTGAGTTAAATTATGTATAAACATAAGTTGCATTAGAAATCAAGC  
ATAAATCACTCAACTGCAAAAAAAAAAAAAAA

## FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ  
HKLRSAVEEMEAEEAAKASSEVNLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG  
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG  
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV  
GSFMEEVROELEDLERSLTEEMALGEPAAAAALLGGEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## **FIGURE 85**

AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCTG  
AAGATAACAATAATTTCAGCCCATCCACTCTCCTTCCCTCCAAACACACATGTGCATGTACACACACATACA  
CACACATACACCTTCTCCTTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGGTCATAGAAAAGGACAC  
TAAAGCCTTAAGGCAGGGCTGGCATTACCTCTGCAGCTCCTTGGCTTGAGTCAGGAAACATGGGAGGG  
CCAGGCACGGTACTCACACCTGTAATCCCAGCATTGGGAGACCGAGGTGAGCAGATCACTTGAGGTCAGGAG  
TTCGAGGACAGGCTGGCAGGAAACATGGAGAAACCCCCATCTACTAAAAAATACAAAAATTAGCCAGGAGTGGTGGC  
AGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCAGGAGAATCGCTGAAATCCAGGAGGGAGGATGCCAGT  
CAGCTGAGTGCACCGCTGCACTCCAGCCTGGGTGACAGAAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA  
GGGTAGATACTGCTTCTGCAACCTCTTAACCTCTGCACTCTCTTCCAGGGCTGCCCCCTGATGGGGCTG  
GCAATGACTGAGCAGGCCAGGAGAACAGGAAGAGAAGGCAAGAGAAGGATATTGAGGAGGGCAAGAAGTGA  
GTGAGAATGACTGCCCTGGGAGGGTCTGGGGCCTGGCAGGGTTGCTGACCCCTACCCCTGCAAAACACA  
AAGAGCAGGACTCCAGACTCTCCTGTGAATGGTCCCCCTGCCCCCTGAGCTCACCATGAGGCTTCTCGTGGCCCC  
ACTCTTGCTAGCTGGGTTGGCTGGTGCCTGCACTGTGCCCCGGTACCCCTGGCATGTTCCCTGCCCCCTCA  
GTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCCGCTGCTTACCGCGAGGCTACCAACTGTGGACTGCAATGA  
CCTATTCTGACGGCAGTCCCCCGGCACTCCCCGAGCACACAGACCCCTGCTGAGGAGCAACAGCATTGT  
CCGTGTGGACCAGAGTGAAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCCAGAACAGCTTTGGA  
TGCCCCAGACTGTGATTTCATGCCCTGCCCCAGCTGCTGAGCCTGCACCTAGAGGAGAACCGAGCTGACCGGCT  
GGAGGACCACAGCTTGCAAGGCTGGCAGCCTACAGGAACACTATCTCAACCACAACCAGCTTACCGCATCGC  
CCCCAGGGCTTTCTGGCTCAGCAACTTGCTGCGGCTGCACCTCAACTCCAACCTCTGAGGGCCATTGACAG  
CCGCTGGTTGAAATGCTGCCAACTGGAGATACTCATGATTGGGGCAACAAGGTAGATGCCATCCTGGACAT  
GAACCTCCGGCCCTGGCCAACCTGCGTAGCCTGGTCTAGCAGGATGAACCTGCGGGAGATCTCGACTATGC  
CCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCCTTCTATGACAACCAGCTGCCCGGGTGCAGGCGGGCACT  
GGAACAGGTGCCGGCTCAAGTCTTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGACTTGC  
CAACATGCTGACCTTAAGGAGCTGGACTGAACAACATGGAGGAGCTGGTCTCCATGACAAGTTGCCCTGGT  
GAACCTCCCCGAGCTGACCAAGCTGGACATACCAATAACCCACGGCTGTCTTCTATCACCCCCCGGCCTTCA  
CCACCTCCCCAGATGGAGAACCTCATGCTCAACAACACGCTCTCAGTGCCTTGCAACAGCAGCGGTGGAGTC  
CCTGCCCAACCTGCAAGGAGGTAGGTCTCCACGGCAACCCATCCGCTGTGACTGTGATCCGCTGGGCAATGC  
CACGGGCAACCGTGTCCGCTTACAGCGGCAATCCACCTGTGCGGAGGCTCCGGACCTCCAGCGCCTCCC  
GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACACTGTTGCCCTCATCTCCCCACGAAGCTTCCCCCAAG  
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCAATTGCCGGCACTGGCCAACCCGAACCCGAGATCTACTG  
GGTCACTCCAGCTGGCTTCGACTGACACCTGCCATGCAGGAGGTACCGGGTAGCCCTGTGAGGAGACAC  
GGAGCTGCGGAGGGTACAGCAGAACAGGAGGGCTATACACCTGTGTTGGCCAGAACCTGGTGGGGCTGACAC  
TAAGACGGTTAGTGTGGTGTGGCGCTGCTCTCCAGCCAGGAGGGAGGAAGGACAGGGCTGGAGCTCCG  
GGTGCAGGAGAACCCACCCCTACACATCTGCTATCTGGTCAACCCACCAACAGTGTCCACCAACCTCAC  
CTGGTCAGTGCCTCCCTCCGGGCCAGGGGCCACAGCTGGCCCTGCCTGGGGAAACCCACAGCTA  
CAACATTACCCGCTCTTCAGGCCACGGAGTACTGGGCTGCCATGCAAGTGGCTTGCTGATGCCACACCA  
GTTGGCTTGTATGGGCCAGGACAAAGAGGGCACTTCTGCCACAGAGCCTAGGGGATGTCCTGGGCTCAT  
TGCCATCCTGGCTCGCTGCTCTCCAGCTGGCAGCTGGCTAGGGCCCACCTTGGCACAGGCCAACCCAGGAA  
GGGTGTGGTGGGAGGGGCCCTCCAGCCTGGCTTCTGGGCTGGAGTGCCTTGCTGGGGTTGT  
GTCTGCTCCCTCGTCTGCCCTGGAAATCCAGGGAGGAAGCTGCCAGATCTCAGAAGGGAGACACTGTTGCC  
ACCATTGTCTAAAATTCTTGAAGCTCAGCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTACAAA  
AGAGAACAGTCTGGGCCAGATGCCCTGCCAGGAAGGGACATGGACCCACGTGCTGAGGGCTGGCAGCTGGC  
CAAGACAGATGGGGCTTGTGGCCCTGGGGTCTGCTGCAGCCTGAAAAAGTTGCCCTACCTCTAGGGTCA  
CCTCTGCTGCCATTCTGAGGAACATCTCAAGGAACAGGGAGGACTTTGGCTAGAGCCTCTGCCCTCCCATCTT  
CTCTGCTGCCATTCTGAGGAACATCTCAAGGAACAGGGAGGACTTTGGCTAGAGCCTCTGCCCTCCCATCTT  
TCTTCTCTGTACAGTCTCAGTTGCTGCTCTGTGCTCTGGCTCCCTGGCAAGGGCTGAAGGGAGGGCACTCCATCTCAC  
CTCGGGGGCTGCCCTCAATGTGGGAGTGACCCAGCCAGATCTGAAGGACATTGGGAGAGGGATGCCAGGAA  
CGCCTCATCTCAGCAGCTGGCTGGCATTCCGAAGCTGACTTTCTATAGGCAATTGTACCTTGTGGAGAA  
ATGTGTCACCTCCCCAACCCGATTCACTCTTCTCTGTAAAAAATAAAATAAAATAACAAATAAAA  
AAAA

## FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDNDLFLTA  
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDSQNSFSDARDCDFHALPQLLSLHL  
EENQLTRLEDHSFAGLASLQEELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMNFRPLANLRSILLAGMNLREISDYALEGLQSLSESLSFYDNQ  
LARVPRALEQVPGKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLP  
ELTKLDITNNPRLSFIHPRAFHHLQPQMELMLNNNALSAHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDQLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ  
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT  
CVAQNLVGADETKTVSVVGRALLQPGRDEGQGLELRVQETHPYHILLSWTPNNTVSTNLTW  
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIAILALAVALLLAAGLA AHLTGQPRKGVGGRPLPPAWAFWGWSAPSVRVV  
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 629-648

**N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

**Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

**Tyrosine kinase phosphorylation site.**

amino acids 532-540

**N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

**Amidation site.**

amino acids 470-474, 660-664, 692-696

## FIGURE 87

GCAAGCCAAGGGCCTGTTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGAGGGGACATTGTGTACCGCCT  
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGCTACTACGTGCACAA  
CATCAAGTTGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCAACCC  
CCTGCCACACTCTTCAGATCCTGGCGTCTTCTACATCAGCTAGTCATCTCTACGGCCTCATCTGCATGTA  
CACACTGTGGTGGATGCTACGGCCTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGCTACAG  
CGACATCCCCGACGTCAAGAACGACTTCGCCTCATGCTGCACCTCATTGACCAATACGACCCGCTACTCCAA  
GCGCTTCGCGCTTCTGCGGAGGTGAGTGAGAACAGCTGCGCAGCTGAACCTCAACAACGAGTGGACGCT  
GGACAAGCTCCGGCAGCGCCTACCAAGAACCGCAGGACAAGCTGGAGCTGCACCTGTCAGTGGCAT  
CCCTGACACTGTGTTGACCTGGTGCAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCGCC  
CAGCATTGCCCAGCTCACGGGCTCAAGGAGCTGTGGCTCTACCAACACAGCGCCAAGATTGAAGCGCCTGCC  
GGCCTTCTGCGCAGAACCTCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCGCTGTGGATCTA  
TAGCTGAAAGACACTGGAGGAGCTGACCTGACGGGCAACCTGAGCGGGAGAACAAACCGCTACATCGTCATCGA  
CGGGCTCGGGGAGCTCAAACGCCCTCAAGGTGCTGGGCTCAAGAGAACCTAAGCAAGCTGCCACAGGTGGTAC  
AGATGTGGCGTGCACCTGAGACTGAGCTGGAGCTGATCCGCTGCACCTGGAGCGCATCCCCACTCCATTTCA  
CCACAAACCTGCAAGGAGATTGACCTCAAGGACAACAACCTCAAGAACCATCGAGGAGATCATCAGCTTCCAGC  
GCACCGCCTCACCGCTTAAGCTGTGGTACAACCACATCGCCTACATCCCCATCCAGATCGGCAACCTCACAA  
CCTGGAGCGCCTCTACCTGAAACCGCAACAAGATCGAGAACGATCCCCACCCAGCTCTTCTACTGCC  
CTACCTGGACCTCAGCCACAACAACCTGACCTTCTCCCTGCCGACATCGGCTCTGCAAGAACCTCCAGAACCT  
AGCCATCACGGCAACCGGATCGAGACGCTCCCTCCGGAGCTTCCAGTGCAGGAGCTGAGCGAGATCGAGCTGCC  
GGGCAACAAACGTGCTGCAGTCAGTCACTGCCCTCCAGGGTGGCGAGCTGACCAACCTGACGCAAGATCGAGCTGCC  
CAACCGCTGGAGTGCCTGCTGTGGAGCTGGCGAGTGCCTCAAGCGCAGCGCTTGGTGGAGGA  
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCGTAGGCC  
GCCGCCAGCACAGCAAGCAGCAGGAGCTGCCAGTCCTCAGGCCGGAGGGGAGGCCCTAGCTTCTCC  
AACTCCGGACAGCCAGGACAGCCTCGCGCTGGCAGGAGCCTGGGCCGCTGTGAGTCAGGCCAGAGCAGA  
GGACAGTATCTGTGGGCTGGCCCTTTCTCCCTGAGACTCACGTCCCCAGGGCAAGTGTCTGTGGAGGAG  
AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGTCTCCTCCCTGGAGGGCAGCTCTGCC  
CTGCCACCAGAGGTCTGGACCCCTCACTTAGTTCTGGTATTATTTCTCCATCTCC  
AGATAACTTATACATTCCAAGAAAGTTGAGCCAGATGGAAGGTGTTCAAGGAAAGGTGGCTGCC  
TTGCTCTTATTAGCGATGCCGCCGGCAATTAAACCCACCTGGACTTCAGCAGAGTGGCTGCC  
CCATGGGACGGTCAACCGCAGTGCCTGGCTGGCTCTGCCGCTGCCAGGGAGAGCAGGCC  
AAGGCCAGGCCCTGGAGCTGCCCTTCAGTTTGCGAGTTAGTTTGTTGGTATT  
AAACAATTAAAAAAAGCTTGGAAATGGATGGTTGGTATTAAAAGAAAAAAACTTAAAAAA  
AAAAGACACTAACGCCAGTGAAGTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTTGAGCAAAGCAGGCC  
TGAACGTGTTCCCTTCCCTGGCGCAGGGTGCAGGGTGTCTTCCGGATCTGGTGTACCTGGTCCAGGAGTT  
CTATTGTTCCCTGGGAGGGAGGTTTTGTTGTTGTTGGTTTTTGTTGGTGTCTTGTGTTCTTCTC  
ATGTGTCTTGGCAGGCACTCATTCTGTGGCTGCGCCAGAGGAATGTTCTGGAGCTGCC  
ACTCGGGTTGGCTAATCCCCGGATGAACCGTGCCTCATTGCACCTCCCTCGCCTGCC  
CGCACAGTGTTAAGGAGCCAAGAGGAGCCACTCGCCAGACTTGTGTTCCCCACCTCC  
CCAGTGCCACCGCTGGCCTCCGCTGCTTCCATGCCCTGCGCACCTGGCTTCA  
GAGGCTGGTGGGAATGGGAGGTGGCCCTGGAGGGCAGGCGTGGTCCAAGGCC  
CTGGAGTGCACACAGCCAGTGCACCTGGTGGCTGGAAGCCAACCTGTTAGAT  
AGAAGGGTCCCCGCTTAGATCAATCACGTGGACACTAAGGCACGTTAGAGTCTTGTCT  
CCATCCGTCTGTCGTCCTTGTGTTCTGCGTGTGTCATTGGATATAATCCT  
CCTCTGACAACCATGAAGAAAAATCCGTTACATGTGGGTCTGAACCTGT  
TAGACTCGGTACAGTATCAAATAAA  
ATCTATAACAGAAAAAA

## FIGURE 88

MRQTIIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI  
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRLQLNLNEWTLDKLRQRLTKNAQDKLELHLFMLSGIPDTVFVLVELEV  
LKLELI PDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFDTIKEIPLWI  
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSPQVVTDVGVHLQKLSI  
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ  
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHGNVLQSLPSRVGELTNLTQIE  
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

**Transmembrane domain:**

amino acids 51-75 (type II)

**N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

**Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

## **FIGURE 89**

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT  
CCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGGCCTGAACGCAGGAGCTGTCAATTGACT  
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG  
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTTGGAAACTTGAGGAAATTGGGC  
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT  
GTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG  
AATTCCAGACAGTTCCATTCTACATTTCTCAGAGTCTATGGAGGAAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCATCAAGTGCAACTTGGGGGG  
TGCCTGGGTGATT CCTGGATCTCCCTGTTGATT CGGTGCTCTCCTGGGGACCTTACCTGT  
ACAGCATGTCTCTCGAACACAAAGGTCTGGCAGAGGTGTCTAAGGGTGCAGAGCAAGTA  
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCCA  
CGTCTACAATGGAGTCAGTCAGATTACACAGAGCCACCTAGTTGTCTTGTCAAGC  
CACGTGAGACACCTACAACGAGATGCCCTAACGCCAGCTCATGAATGGCCCCATCAGAAAGAA  
GCTAAAATTATTCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC  
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAAGGAGGC  
GGTGCAGAAACTGAAGTGGCCAGAACTGCCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCC  
ACAGTGAACCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC  
TACTGGATTCTGAAAGCTGGTCATATGGTCCCTCTGACCAAGGGACATGGCTCTGAAGAT  
GATGAGACTGGTGAECTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGC  
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT  
AACTGGGGCTGTGATCAAGAACAGGTTCTGACCAAGCTCTGCAGAGGATAAAATCATTGTCT  
GGAGGCAATTGGAAATTATTCTGCTTCTAAAAACCTAAGATTTTAAAAAATTGAT  
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

## FIGURE 90

MELALRRSPVPRWLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE  
ATELGKAEMIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWVRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP  
SDQGDMALKMMRLVTQQE

**Signal sequence:**

amino acids 1-25

**N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

**Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

**N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## **FIGURE 91**

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGGCCGA  
CGGGTCATCACGTGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA  
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG  
CACTCACGGCGGCGCACTGCTTGAAACCTATAGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTGGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG  
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGATTCAACCTATGACATTG  
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG  
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA  
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTGCCATCATAAACAA  
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCGCAAGGACATCTTGGAGACATG  
GTTTGTGCTGGCAACGCCAAGGCGGGAGGATGCCTGCTCGGTGACTCAGGTGGACCCTT  
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGCTGTG  
GTCGCCCAATCGGCCGGTGTCACCAATATCAGCCACCATTGAGTGGATCCAGAAG  
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTCCCTCT  
TCTCTGGCTCTCCACTCCTGGGCGGTCTGAGCCTACCTGAGCCCATGCAGCCTGGGC  
CACTGCCAAGTCAGGCCCTGGTTCTCTGTCTTGTAAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAA

1000 900 800 700 600 500 400 300 200 100

## FIGURE 92

MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPQGSLRLW  
DSHVCGVSLLSHRWALTAACFETYSDELSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG  
LWYQIGVVSWGVGCGRPNRPGVYTNIHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

**Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

**N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

**Amidation site.**

amino acids 33-37

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

**Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

## FIGURE 93

CCCCACGCGTCCGGACGCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCTAGGGCT  
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCGGAGCCGACCAGCGAGGACGC  
TGCCCCCAGGCTGGGTGCCCCCTGGGCGTGCAGGACCCCTGAGGAAGAGCTGAGTCACCTT  
GCCCTGAGACAGCAGAATGTGAAAGACTCTCGGAGCTGGTGCAGGCTGTGAGGATCCCAG  
CTCTCCTCAATAACGGAAAATACCTGACCCCTAGAGAATGTGGCTATCTGGTGGAGGCCATTCC  
CACTGACCCCTCCACACGGTGCAGGGAAATGGCTCTTGGCAGCCGGAGCCAGAAGTGCATTCT  
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATTGACAAGCAGAGCTGCTGCTCCC  
TGGGGCTGAGTTCATCACTATGTGGGAGGACCTACGGAAACCATGTTGTAAGGTCCCCAC  
ATCCCTACCAGCTTCACAGGCCTTGGCCCCCATGTGGACTTGTGGGGGACTGCACCGT  
TTTCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGAGGTGACAGGGACTGTAGGCCT  
GCATCTGGGTAACCCCTGTGATCCGTAAGCGATAACAACCTGACCTACAAGACGTGG  
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCCCTGGAGCAGTATTCCATGAC  
TCAGACCTGGCTCAGTTCATGCGCCTTCGGTGGCAACTTGACATCAGGCATCAGTAGC  
CCGTGTGGTGGACAACAGGGCCGGGGCCGGGATTGAGGCCAGTCTAGATGTGCAGT  
ACCTGATGAGTGCTGGTGCACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG  
GGACAGGAGCCCTTCCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT  
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCCCTACATCCAGCGGGTCA  
ACACTGAGCTCATGAAGGCTGCCCTGGGTCTCACCCCTGCTCTCGCCTCAGGTGACAGT  
GGGGCCGGGTGTTGGCTGTCTGGAAAGACACCAAGTTCCGCCCTACCTTCCCTGCCCTCCAG  
CCCCTATGTCACCACAGTGGAGGCACATCCTCCAGGAACCTTCCTCATCACAAATGAAA  
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCACGGCCTTCATACCAGGAG  
GAAGCTGTAACGAAGTTCTGAGCTAGCCCCCACCTGCCACCATCCAGTTACTTCAATGC  
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACTTCTGATGGCTACTGGGTGGTCAGCAACA  
GAGTGCCATTCCATGGGTGTCGGAACCTCGCCTCTACTCCAGTGGTTGGGGGATCCTA  
TCCTGATCAATGAGCACAGGATCCTAGTGGCCCCCCCTTGGCTTCTCAACCCAAG  
GCTCTACCAGCAGCATGGGCAGGTCTTTGATGTAACCGTGGCTGCCATGAGTCCTGTC  
TGGATGAAGAGGTTAGAGGGCCAGGGTTCTGCTCTGGCTGGCTGGATCCTGTAACAGGC  
TGGGGAACACCAACTCCCAGTTGCTGAAGACTCTACTCAACCCCTGACCCCTTCCTATC  
AGGAGAGATGGCTTGTCCCCCTGCCCTGAAGCTGGCAGTTCAAGTCCCTTATTCTGCCCTGTTG  
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA  
TGCTGTGAGCTTGACTTCAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT  
CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTTTGATGCTCTCCCTCCGC  
ATCTCATCTTCTCTTCAATCAGGCTTTCCAAGGGTTGTATACAGACTCTGTGCACCA  
TTCACTGATATTCACTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT  
TTCCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTGTGTTATG  
GCCTTCCATCATAGTTGCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACCTCTG  
ACTACTCTTGTCTTCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTG  
TCCATTGTAGATTTGCTCTCAGTTACTCATTGCCCCCTGGAACAAATCACTGACA  
TCTACAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATAACCTCAA  
TGTAAAAAA

## FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL  
SIRQAELLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLRQRP  
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYIAMSAGANISTWVYSSPGRHEGQEPMFLQWML  
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLFASGDSGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP  
HLPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG  
RPPLGFLNPRLYQQHGAGLFDVTRGCHECLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

**Signal sequence:**

amino acids 1-16

**N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

**Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

**Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

**N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

## FIGURE 95

GGCGCGCGCTCTCTCCGGGCCACACCTGTCTGAGCGGCGAGCGAGCCGGCCGGC  
GGGCTGCTCGCGCGAACAGTGCTCGCATGGCAGGGATTCCAGGGCTCCTCTCCTCTC  
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTACAGTGCCCCCTGAAACCCACTTG  
GCCTGCATAACCGCCTCCCTGCGTCTGCCCCAGTCTACCCCTCAATTAGCCAAGCCAGACT  
TTGGAGCCGAAGCAAATTAGAAGTATCTTCATGTGGACCCCAGTGTCTAAGGGAACCT  
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG  
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC  
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC  
AGGTTCAGCATTGGAGGGACTTCCTGCTCAACTACCCTTCTCAACATCAGTGAAGTT  
ATCCACGGGCTGCACCGCACCCCTGGTGGCAGAGAACGATGTCTCACAGCTGCCACTGCA  
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAACGACTCCACTTCAGCCATGCCAGCAGATGAA  
AAGTTAAAGATGGTGGTCGAGGGCCAACGACTCCACTTCAGCCATGCCAGCAGATGAA  
ATTCAGTGGATCCGGGTGAAACGCACCCATGTGCCAAGGGTGGATCAAGGGCAATGCCA  
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACCTAAAAAGCCCCACAAGAGAAAA  
TTTATGAAGATTGGGGTGAGCCCTCGCTAACGAGCTGCCAGGGCAGAATTCAACTTCTC  
TGGTTATGACAATGACCGACCAGGCAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA  
CCTATGACTTGCTCTACAGCAATGCGATGCCAGCCAGGGCCAGCGGGTCTGGGTCTAT  
GTGAGGATGTGGAAGAGACAGCAGCAGAACGTTGAGCGAAAAATTATTGGCATTTCAGG  
GCACCAAGTGGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAATCACTC  
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG  
TGACACAGTGTCCCTGGCAGCAATTAAGGGCTTCAATTGTTCTTATTTAGGAGAGGCC  
AAATTGTTTGTCAATTGGCGTGCACACGTGTGTGTGTGTGTGTGTAAAGGTGT  
CTTATAATCTTACCTATTCTACAATTGCAAGATGACTGGCTTACTATTGAAAATG  
GTTTGTGTATCATATCATATCATTAAAGCAGTTGAAGGCATACTTTGCATAGAAATAA  
AAAAAAACTGATTGGGCAATGAGGAATATTGACAATTAAGTTAATCTCACGTTTG  
CAAACTTGATTTATTCATCTGAACATTGTTCAAAGATTATTAATATTAAATATTGGCATA  
CAAGAGATATGAAAAAAAAAAAAAA

## **FIGURE 96**

MAGIPGLLFLLFFLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA  
KPDFGAEAKLEVS  
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRD  
SGSSGKS  
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTA  
AHCIDHGKTYVKG  
TQKLRVGFLKPKFKDGGRGANDSTSAMPEQMFKQWIRVKRTHVPKG  
WIKGNA  
NDIGMDYDYA  
LLELKPKH  
RKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDV  
KDETYDLYQQCD  
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWDMNGSPQDFNV  
AVRITPLKYAQICYW  
IKGNYLDCREG

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 93-97, 207-211

**Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

**Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

**N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

**Serine proteases, trypsin family, histidine active site.**

amino acids 171-177

## FIGURE 97

GCATGCCCTGGGTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT  
CTGGAGCGCCCCCAGCCCTGGGTGGGGCTGTCTCGCACCTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCAGCCTGTGGAAAGCCCCA  
GCAGCTGAACC GGTTGTGGCGGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACC ACTGCGCAGGTTCTGCTCACCA GCGCTGGGTGATC  
ACTGCTGCCCACTGTTCAAGGACAACCTGAACAAACCATACTGTTCTGCTGCTGCTGGG  
GGCCTGGCAGCTGGGAACCCCTGGCTCTGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC  
CCCACCTGTGTATTCTGGAAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGCCTGCCATCTGCCCTACCTGATGCCCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTCCCTTGC  
CCCACCTCAGACCCCTGCAGAACAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT  
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCCCTATGTGCCAGGTGGACG  
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGCGAGGGCTGTGCCAGCGAACAGGCC  
GGGGTCTACATCAGCCTCTGCGCACCGCTCTGGTGGAGAAGATCGTCAAGGGGTGCA  
GCTCCGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCCG  
CCGCGCGCTCCTAGGGCGCAGCGGGACGCGGGCTGGATCTGAAAGGCGGCCAGATCCACA  
TCTGGATCTGGATCTGCGCGGCCTCGGCGGTTCCCCCGCCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCGGACGGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCGAC  
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGCCAACGGCCTCATGTCCCCGCCCCAC  
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTGTATATAATGTTAATGATTTTAT  
AGGTATTTGTAACCCTGCCACATATCTTATTATTCCCTCCAATTCAATAATTATTATT  
CTCCAAAAAAA

## **FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318  
><subunit 1 of 1, 317 aa, 1 stop  
><MW: 33732, pI: 7.90, NX(S/T): 1  
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP  
WIVSIQKNGTHHCAGSLLTSRWVITAHCFKDNLNKPYLFVLLGAWQLGNPGSRSQKVGVVA  
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG  
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC  
QVDGAWLLAGII SWGEGCAERNRPGVYISLSAHRSWEKIVQGVQLRGRAQGGGALRAPSQG  
SGAAARS

**Signal sequence:**

amino acids 1-32

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## **FIGURE 99**

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTCCCTGATGCTCTGCTGCCGCTACTGCTA  
CTGCTGGTGGCCACCACAGGGCCCAGTGGAGCCCTCACAGATGAGGAGAAACGTTGATGGT  
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTCACATGA  
GATGGGACGAGGAGCTGGCCGCCTCGCCAAGGCCTACGCACGGCAGTGCCTGGGGCAC  
AACAAAGGAGCGCGGGCGCCGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGT  
GCCGCTGGCCATGGAGGAGTGGCACCAACGAGCGTGAGCACTACAACCTCAGGCCGCCACCT  
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC  
GGCTGTGGTCCCCACTTCTGTGAGAAGCTCCAGGGTGGTGGAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGGCCCTACCAGGAGGGACTC  
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC  
CCGGAAGATGCTCAGGATTTGCCTTACCTGGTAAC TGAGGCCCCATCCTCCGGCGACTGA  
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTCCCTAGCAACGGGGATTCCGGCTTTCT  
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC  
CCAACTTCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTGCGTAAC  
AACTGAGGTCCCTCCATTGGCAGCTCACAGCCTGCCCTCCTGGATGAGGAGCCAGTTA  
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA  
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTGGACCCCAAGATGTCCCTGACAGGGCAAG  
GGAACTCCTACCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCAGTG  
AGGTCTTGGCCTCAGTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGTCTGCCAGGTGCAGAGGGCCCTGACA  
AGCCTAGCGTTGTGTCAAGGCTGAACCTGGCCCTGGTCATGTGTGGGGCCCTCCCTGGGA  
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTTGAATGGGATACCAACTCAAAGGG  
TGAAGAGGTCACTGTCCTCTGTCACTTCCCCACCCCTGTCCCCAGGCCCTAAACAAGATA  
CTTCTTGGTTAAGGCCCTCCGGAAAGGAAAGGCTACGGGCATGTGCCCTCATCACACCCTCC  
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC  
GGGCCACACCTCCTGCCCTCCCTGAGTCCTGGGGTGGAGGATTGAGGGAGCT  
CACTGCCTACCTGGCCTGGGCTGTCTGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG  
TGTAGCTGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTC  
TTTGAGTGGGGAGGCAGGGACGAGGAAGTAACCTGACTCTCCAATAAAACCT  
GTCCAACCTGTGAAA

## **FIGURE 100**

MHGSCSFLMLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE  
LAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMVDPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGETPCSQC  
PSGYHCKNSLCEPIGSPEADAQDLPYLVTTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV  
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAGHSILPSLDEEPVTFPKS  
THVPIPKSADKVTDKTKVPSRSPENSIDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV  
SGLNSGPGHVWGPLLGLLLPPLVLAGIF

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

## **FIGURE 101**

GTAACGTGAGTCAGGCTTTCATGGGAAGCCCCCTCAACAGAACCGGACTTAAGTCACAACAGATTATCTTCAAGTTATGGTGGACGT  
ACTTCTGTTCTCCCTGCTTACATTAGCAGACGGACTTAAGTCACAACAGATTATCTTCA  
CAAGGCAAGTCCATGAGCCACCTTCAAAGCCTCGAGAAGTGAACACTGAACAACAAATGAATTGGAGACCATTCC  
AAATCTGGGACCAAGTCTCGGCAAATATTACACTTCTCCTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA  
ACATCTGAAAGAGTTCACTCCCTGAAACTTGGACCTAGCAGAACAAATATTCAAGAGCTCCAAACTGCATT  
TCCAGCCCTACAGCTCAAATATCTGTATCTCACAGAACCGAGTCACATCAATGGAACCTGGTATTTGACAA  
TTTGCCAACACACTCCTGTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAAGATGTTAAACT  
GCCCAACTGCAACATCTGAATTGAACCGAAACAAGATTAAAGTAGATGGACTGACATTCCAAGGCCTGG  
TGCTCTGAAAGTCTGAAATGCAAAGAAATGGAGTAACGAAACTATGGATGGAGCTTTGGGGCTGAGCAA  
CATGAAATTTGAGCTGGACCATAACAAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGCTGATGCT  
GCAGGAACCTCATCTCAGCCAAAATGCCATCACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAACGCTCAG  
TGAGCTGGACCTAACCTCAATCACTTCAAGGTTAGATGATTCAAGCTTCTGGCCTAAGCTTAACAAATAC  
ACTGCACATTGGAAACAAACAGTCAGCTACATTGCTGATTGCTGCTTCCGGGGCTTCCAGTTAAAGACTTT  
GGAGTGAAGAACATGAAATTCTCGGACTATTGAGACATGAATGGTCTTCTCTGGGCTTGACAAACTGAG  
GCGACTGATACTCCAAGGAAATCGGATCCGTCTTAACTAAAAAGCCTTACTGGTTGGATGCAATTGGAGCA  
TCTAGACCTGAGTGAACACGCAATCATGTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAAATT  
GCATTAAATACATCAAGCTTTGCGATTGCCAGCTAAATGCCATCAGCTTGGGGGGAAACAAACTT  
TCAGAGCTTGAAATGCCAGTTGCTGCTTCCAGCTTAAAGGAAAGAACGATTGGCTGTTAGCCCAGA  
TGGCTTGTGTGATGATTTCACAAACCCAGATCACGGTCAGCCAGAACACAGTCGGCAATAAAAGGTT  
CAATTGAGTTCATCTGCTCAGCTGCCAGCAGTCAGTATTCCAAATGACTTTGCTTGGAAAAAAAGACAATGA  
ACTACTGCATGATGCTGAAATGGAAATTATGACACACCTCCGGGCCAAGGTTGGCGAGGTGATGGAGTATACCAC  
CATCCTCGGCTGCGAGGTGGAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAATCACTTTGGTC  
ATCCTACTCTGCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCAACAGACCCCCATGGATCTCACC  
CCGAGCTGGGGCATGGCACGCTGGAGTGCTGCTGCTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAC  
TGGGGGACAGACTTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCGAGGATGACGTGTTTATCGT  
GGATGTGAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTCAAGCAAATGC  
AACTCTGACTGCTAGAACACCATCATTTCAGGCCACTGTTGGACCGAAGTGAACCAAGGGAGAACAGC  
CGTCTACAGTGCATTGCTGGAGGAAGGCCCTCCCTAAACTGAACCTGGACCAAAGATGATAGCCCATTGGTGG  
AACCGAGAGGCACTTTTGAGCAGGCAATCAGCTTCTGATTATTGAGACTCAGATGTCAGTGTGCTGGAA  
ATACACATGTGAGATGCTAACACCCCTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCA  
CTGCGACTCCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGATCATAG  
CGTGGTTGCTGTGGGGCACGTCACTCGTGTGGGTGATCATACACACACAAGGCGGAGGAATGAAGA  
TTGCAGCATTACCAACACAGATGAGACCAACTGCCAGAGATATTCTAGTTATTGTCATCTCAGGAACGTT  
AGCTGACAGGCAGGATGGTACGTGTTCAAGAAAGTGGAAAGCCACACCAGTTGTCACATCTCAGGTGCTGG  
ATTTTCTTACACACATGACAGTAGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAGCTGC  
CACAGATCTGTTCTTGCGTTTGGGATCCACAGGCCCTATGTATTGAAAGGAAATGTGATGGCTCAGA  
TCCTTGTAAACATATCATACAGGTTGCACTGCCAGAACAGTAAATGGACCAACTATGAGGCCAGTT  
CATAAAGAAAAAGGAGTGCCTACCCATGTTCTCATCCTCAGAAGAACCTGCCAGGGAGCTCAGTAATATATC  
GTGGCCTTCACATGTGAGGAAGCTACTAACACTAGTTACTCTCACAAATGAAGGACCTGGAATGAAAATCTGTG  
TCTAAACAAGTCTCTTAAAGTTAGTTAGTGCACATCCAGGCCAGGGCTGGTGCCTCGAGTAATTCTTATGG  
TACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCTTATTCAAGCTTGGACAGCCATCAGATTGTGAGCC  
AAGAGCCTTTATTGAAAGCTCATCTTCCCAAGACTTGGACTCTGGGTGAGAGGAAGATGGAAAGAAAGGAC  
AGATTTCAGGAAGAAAATCACATTGTACCTTAAACAGACTTTAGAAAATACAGGACTCCAAATTTCAGTC  
TTATGACTGGACACATAGACTGAATGAGACCAAGGAAAAGCTTAACACATACACTCACAGTGAACCTTATT  
AAAGAGAGAAATCTTATGTTAAATGGAGTTATGAATTAAAGGATAAAATGCTTATTATACAGAT  
GAACCAAATACAAAAGTTATGAAAATTAAACTGGGAATGATGCTCATATAAGAATACCTTTAAACTA  
TTTTTAACTTGTGTTATGAAAAAGTATCTACGTAATTAAATGATATAATCATGATTATTTATGTATT  
TTATAATGCCAGATTCTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGACCATT  
TTAAATAGAAGTTACTTCATTATTTGCACATTATTAATAAAATGTGCAATTGAA

## FIGURE 102

MVDVLLLFSLCLLFHISRPDLHNRLSFIKASSMSHLQLSLREVKLNNNELETIPNLGPVSAN  
ITLLSLAGRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP  
GYFDNLANTLLVLKLNRRNRIASAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKM  
QRNGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLGYLLMLQELHLSQNAINRISPDAWE  
FCQKLSLEDDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDLKNNE  
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ  
MKKLQQLHLNTSSLLCDCQLKWLPOWVAENNQSFVNASCAPQLLKGRSIFAVSPDGFVCD  
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQG  
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVAKLTVNMLPSFTKTPMDLTIRAGA  
MARLECAAVGHPAPQIAWQKDGTDFFPAARERRMHVMPEDDVFIVDVKIEDIGVYSCTAQN  
SAGSISANATLTVLETPSFLRPLLDRVTKGETAVLQCIAGGSPPPKNWTKDDSPPLVVTER  
HFFAAGNQLLIIVDSDVSDAGKYTCMSNTLGERGNVRLSVIPTPTCDSPQM TAPS LDDDG  
WATVGVIIIAVVCVVGTSLVWVVIYHTRRRNEDCSITNTDETNL PAD I P SYL SS Q GT LAD  
RQDG YVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATD LFLCPFLGSTGP  
MYLKGNVYGS DP FETYHTG C PDPRTVLM DHYE PSYIKK KECYPC SHP SEES CERS FSN ISW  
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA  
YSSFGQPSDCQPR AFYLKAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTLEN YRTPNFQS  
YDLDT

**Signal sequence:**

amino acids 1-19

**Transmembrane domain:**

amino acids 746-765

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGGCTTGCACAAATG  
AAGGATGCAGGACGCAGCTTCTCTGGAACCGAACGCAATGGATAAAACTGATTGTGCAAGAGAGAAGGAAGAAC  
GAAGCTTTCTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA  
TAAACCAGAGTAGACCCGCGGGGTTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTGTTCCCCCTCC  
CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCAAAGAAAAAGTATGTTCTTTTCTC  
TATAAAGGAGAAAGTGAGGCCAAGGAGATATTTGGAATGAAAGTTGGGCTTTTAGTAAAGTAAGAAACT  
GGTGTGGTGGTGTTCCTTCTTTGAATTCCCACAAGAGGAGAGGAAATTAAATAACATCTGCAAAGAAA  
TTTCAGAGAAGAAAAGTTGACCGCGCAGATTGAGGCATTGATTGGGGAGAGAACACCAGCAGAGCACAGTTGGA  
TTTGTGCTATGTTGACTAAAATTGACGGATAATTGCAAGTGGATTTCATCAACCTCCTTTTTAAAT  
TTTATTCCCTTGGTATCAAGATCATCGCTTCTCTTCTTAAACCACCTGGATTCCATCTGGATGTTGCT  
GTGATCAGTCTGAAATACAACACTGTTGAATTCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGAT  
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCATTGACCCCTGCTTGTGGTGT  
GCTGGCTCTCAACTCTGTGGTGGCTGGCTGGTGGGGCTCAGACCTGCCCTCTGTGCTCTGAGCAA  
CCAGTTCAAGGTGATTGTGTCGGAAAAACCTCGCTGAGGTTCCGGATGGCATCTCCACCAACACAGGCT  
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCACTTGAGGCATTGAAATCCT  
ACAGTTGAGTAGGAACCATATCAGAACCATATTGAAATTGGGGCTTCAATGGTCTGGCAACCTCAACACTCTGGA  
ACTCTTGACAATCGTCTACTACCACATCCCAGTGGAGCTTTGATACTTGTCTAAACTGAAGGAGCTCTGTT  
GCGAAACAACCCATTGAAAGCATCCCTTCTTATGCTTTAACAGAATTCCCTTTGCGCCGACTAGACTTAGG  
GGAATTGAAAAGACTTCATACATCTCAGAAGGTGCCTTGAAGGTCTGTCCAACCTGAGGTATTGAAACCTTGC  
CATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAACTAGATGAGCTGGATCTTCTGGGAAATCA  
TTTATCTGCCATCAGGCTGGCTTTCCAGGGTTGATGCACCTCAAAACTGTGGATGATACAGTCCCAGAT  
TCAAGTGATTGAACGGAATGCCATTGACAACCTTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC  
ATTACTGCCTCATGACCTTCACTCCCTGATCATCTAGAGCGATACATTACATCACACCCCTGGAAACTG  
TAACGTGACATACTGTGGCTCAGCTGGGATAAAAGACATGGCCCCCTGAACACAGCTGTTGTGCCGGTG  
TAACACTCCTCCAATCTAAAGGGAGGTACATTGGAGAGCTGACCAGAATTACTTCACATGCTATGCTCCGGT  
GATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAGGCATGGCAGCTGAGCTGAAATGTCGGCCTCCACATC  
CCTGACATCTGATCTGGATTACTCCAAATGGAACAGTCATGACACATGGGCGTACAAAGTGC GGATAGCTGT  
GCTCAGTGTGGTACGTTAAATTCAAAATGTAACCTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA  
TTCCGTTGGAAACTACTGCTTCAGCCACCTGAGGATGTCAGCAACCCTACTCCTTCTCTTACTTTTCA  
AACCGTCACAGTAGAGACTATGGAACCGCTCAGGATGAGGACGGACACAGATAACAAATGTGGGCCCCACTCC  
AGTGGTCAGTGGAGACCAATGTGACCCCTCTCACACCAACAGAGCACAGGGCGACAGAGAAAACCTT  
CACCATCCCAGTGAATGATATAAACAGTGGATCCCAGGAATTGATGAGGTCTGAAGACTACAAAATCATCAT  
TGGGTGTTTGTGCCATCACACTCATGGCTGCAGTGATGCTGGTCTTACAAAGATGAGGAAGCAGCACCA  
TCGGCAAAACCATCACGCCAACAGGACTGTTGAAATTATTAAATGTGGATGATGAGATTACGGGAGACACACC  
CATGGAAAGCCACCTGCCATGCCGTCTATGAGCATGAGCACCTAAATCACTATAACTCATCAAATCTCCCTT  
CAACCAACAAACAGTTAACACAATAATTCAATACACAGTTCACTGATGCAACCGTTATTGATCCGAATGAA  
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGAGTTACAAAAAAACAAACAATCAAAAAAAA  
GACAGTTATTAAAAATGACACAAATGACTGGCTAAATCTACTGTTCAAAAAGTGTCTTACAAAAAAACAA  
AAAAGAAAAGAAATTATTATTAAAGCAGACAAAA

## FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRLNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWCNCNDIL  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE  
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVNSVGN  
TTASATLNVTAATTPFSYFSTVTETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ  
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN  
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYN SYKSPFNHTTVNTINSIHSS  
VHEPLLIRMN SKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537

## **FIGURE 105**

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTCGGTTCCCTCTGCTGTTGGGGCA  
TGAAAGGGCTTCGCCCGGGAGTAAAAGAAGGAATTGACCGGGAGCGCGAGGGAGGAGCGCGCACCGCACCG  
GAGGGCGGGCGTGCACCTCGGCTGGAGTTGTGCCGGGCCCCAGCGCGCCGGCTGGAGCTGGTAGA  
GACCTAGGCCGCTGGACCGCGATGAGCGCGCCGAGCCTCCGTGCCGCCGGGGTTGGGAGCTGGTAGA  
GCGGTGCTGGGGCGCGCTGGCCGCTCGACAGCGGGCGTGCAGGGAACTCGGGCAGCCCTCTGGGAGCTGGTAGA  
GAGCGCCCAGTCCCCACTACCTGCCGCTGCCCTGGGGACCTGCTGGACTGCACTGTAAGCGGCTAGCGCTCTT  
CCCGAGCCACTCCCGTCTGGTGCCTGGACTTAAGTCACAACAGATTATCTTCATCAAGGCAAGTCC  
ATGAGCCACCTCAAGCCTCGAGAACAGTGAACACAATGAATTGGAGACCAATTCAAATCTGGGACCA  
GTCTCGGAAATATTACACTTCTCTTGGCTGAAACAGGATTGTGAAGAAATACTCCCTGAACATCTGAAAGAG  
TTTCAGTCCCTGAAACTTGGACCTTAGCAGCAACAAATATTCAAGGCTCAGCAGCTCCAAACTGCAATTCCAGCCCTACAG  
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACTGGGTTAGTGAACATTGGGAAACACA  
CTCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTAAACTGCCCCAACTGCAA  
CATCTGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCTTGGTGCCTGAAAGTCT  
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAACATGGAAATTG  
CAGCTGGACCATAACACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTGCTGATGCTGCAGGAACATTCA  
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCTGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA  
ACTTCATCAACTTATCAAGGTTAGATGATTCAAGCTTCTGGCCTAAGCTTACTAAATACACTGCACATTGG  
AAACAACAGAGTCAGCTACATTGCTGATTGTGCCCTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAAGAAC  
AATGAAATTCTCTGGACTATTGAAGACATGAATGGTCTTCTGGGCTTGACAAACTGAGGCGACTGATACTC  
CAAGGAAATCGGATCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCATTGGAGCATAGACCTGAGT  
GACAACGCAATCATGTCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAAATTGCAATTAAATACA  
TCAAGCCTTTGTGCATTGCCAGCTAAATGGCTCCCACAGTGGTGGCGAAAACAATTTCAGAGCTTGT  
AATGCCAGTTGTGCCATCCTCAGCTGCTAAAGGAAGAACGATTGGTCTGTTAGCCAGATGGCTTGT  
GATGATTTCCAAACCCAGATCACGGTTAGCCAGAAACACAGTCGGCAATAAAAGGTTCAATTGAGTT  
ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTGCTTGGAAAAAGACAATGAACACTGCATGAT  
GCTGAAATGGAAAATTATGCACACCTCCGGGCCCCAAGGTGGCGAGGTGATGGAGTATACCACCATCCTCGGCTG  
CGCGAGGTGGAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCCAATCACTTGCTTCACTCTGTC  
AAAGCCAAGCTTACGTAATATGCTTCCCTCATTCCAAGACCCCCATGGATCTCACCATCCGAGCTGGGCC  
ATGGCACGCTGGAGTGCTGCTGGGCAcccAGCCCCAGATAGCCTGGCAGAAGGATGGGGCACAGAC  
TTCCAGCTGCCAGGGAGAGACGCATGCTGATGCCAGGATGAGCTTCTTCTGGAATGTGAAGATA  
GAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAAGGAAGTATTCAGCAATGCAACTCTGACTGTC  
CTAGAAACACCATCATTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCCTCACAGTGC  
ATTGCTGGAGGAAGGCCCTCCCCCTAAACTGAACTGGACCAAGATGATAGCCATTGGTGGTAACCGAGAGGCAC  
TTTTTGCAAGCAGGCAATCAGCTCTGATTATTGTGGACTCAGATGCTGAGCTGGAAATACACATGTGAG  
ATGCTAAACACCTTGGCACTGAGAGAGGAAACGTGCCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCT  
CAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGCTGATCATAGCCGGTTGT  
GTGGGGCACGTCACTCGTGTGGGTGATCATATAACCACACAAGCGGAGGAATGAAGGATGGCAGCATTACC  
AACACAGATGAGACCAACTGCCAGCAGATTCCCTAGTTATTGTCATCTCAGGGAACGTTAGCTGACAGGCAG  
GATGGGTACGTGCTTCAAGAAAGTGAAGGCCACCAAGCTTGTACATCTCAGGTGCTGGATTTCCTTACCA  
CAACATGACAGTAGTGGACCTGCCATATTGACAATAGCAGTGAAAGCTGATGTGAAGCTGCCACAGATCTGTC  
CTTGTGCTGTTGGGATCCACAGGCCCTATGTATTGAAGGGAAATGTGTATGGCTCAGATCCTTGTAAACA  
TATCATAACAGGTTGCACTGCCAGCAGAAACAGTTAATGGACCACTATGAGCCAGTTACATAAAAGAAAAG  
GAGTGTACCCATGTTCTCATCCTCAGAAGAATCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTCACAT  
GTGAGGAAGCTACTTAAACACTAGTTACTCTCACAATGAAGGACCTGGAAATGAAAAATCTGTGCTAAACAAGTCC  
TCTTAGTTTGTGCAATCCAGAGGCCAGCGTGGCTGCTCGAGTAATTCTTCTATGGTACCTTGGAAAAA  
GCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACGCCATCAGATTGTCAAGGCAAGAGCCTTAT  
TTGAAAGCTCATTCTCCCGAGACTGGACTCTGGGTCAAGGAGAAGGGAAAGAAAGGAGAGGAGATTTTCA  
GAAAATCACATTGTACCTTAAACAGACTTAGAAAACAGCTTAACATACACCTCAAGTGAACTTTTATTAAAGAGAGGAGAAT  
ACATAGACTGAATGAGACCAAGGAAAAGCTTAACATACACCTCAAGTGAACTTTTATTAAAGAGAGGAGAAT  
CTTATGCAAAAAGTATCTTACGTAATTAAATGATGCTCATATAAGAATACCTTTTAAACTATTTTAACTT  
AAAAAGTTATGAAATTTTATACTGGGAATGATGCTCATATAAGAATACCTTTTAAACTATTTTAACTT  
TTTATGCAAAAAGTATCTTACGTAATTAAATGATGATTATTATGTTATGTTATAATGCCAGA  
TTCTTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCATTTTAAATAGAAGTT  
ACTCATTATATTGCACATTATAATAATGTGCAATTGAAAAAAAAAAAAAA

## FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCTTCRCLGDLDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQLSREVKLNNELETIPNLGPVSANIT  
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY  
FDNLANTLLVLKLNRRNRIISAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR  
NGVTKLMGAFWGGLSNMEILQLDHNNLTEITKGWLGYGLLMLQELHLSQNAINRISPDAWEFC  
QKLSELDLTNFNHLRLDDSSFLGLSLLNLTIGHNNRVSYIADCAFRLGSSLKTLDLNNEIS  
WTIEDMNGAFSGLDKLRRRILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK  
KLQLQHLNTSSLCDCKWLPPQWVAENNQSFVNASCAPQLLKGRSIFAVSPDGVCDDF  
PKPQITVQPETQSAIKGSNLSFICSAASSSDPMTFAWKKDNELLHDAEMENYAHLRAQGGE  
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA  
RLECAAVGHPPAQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA  
GSISANATLTVLETPSFLRPLLDRVTKGETAVLQCIAGGSPPPMLNWTKDDSPLVTERHF  
FAAGNQLLIIVDSDVSDAGKYTCMSNTLGTERGNVRSLVIPTPTCDSPQMTAPSLLDDGWA  
TVGVVIIAVVCCVVGTSLVWWVIIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTLADRO  
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY  
LKGNVYGSDPFETYHTGSPDPRTVLMHDYEPSYIKKKECYPCHPSEESCRSFSNISWPS  
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS  
SFGQPSDCQPRAFYLAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYLDLT

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
1073-1077, 1079-1083, 1081-1085

**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

**Leucine zipper pattern.**

amino acids 58-80, 65-87

## **FIGURE 107**

CAAAACTTGCCTCGCGGAGAGGCCAGCTGACTTGAATGGAAGGAGCCCAGGCCGGAGCGCAGCTGAGAC  
TGGGGGAGCGCGTTCCGGCCTGTGGGCGCCTCGGCCGGGGCGCAGCAGGAAGGGGAAGCTGTGGTCTGCC  
CTGCTCCACGAGGCGCCACTGGTGTGAACCAGGGAGAGCCCCCTGGTGGTCCCGTCCCCTATCCCTCTTATATA  
GAAACCTTCCACACTGGGAAGGCAGCGCGAGGAGGGCTCATGGTGAGCAAGGAGGCCGGCTGATCTGCAG  
GCGCACAGCATTGGAGTTACAGATTTACAGATACCAAATGGAAGGCAGGGAGGCAGAACAGCCTGCCCTGGT  
TCCATCAGCCCTGGCGCCAGGCGCAGCTGACTCGGCACCCCTGCAGGCACCATGGCCAGAGGCCGGGTGCTGC  
TGCTCCTGCTGCTGCGCCACAGCTGCACCTGGGACCTGTGCTTGCGTGGAGGAGGCCAGGATTTGGCCGAA  
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTGCGGAGGAGGCCGGTGTGACTGAGCCCTGAGG  
AGCCCCGGCTGGCCAGCCGGTCAGCTGCCCGAGACTGTGCTGTTCCAGGAGGGCGTGTGGACTGTG  
GCGGTATTGACCTGCGTGAAGTCCCCGGGGACCTGCCTGAGCACACCAACCCATCTCTGCAGAACAAACCAGC  
TGGAAAAGATCTACCCCTGAGGAGCTCTCCGGCTGCACCCGGCTGGAGAACACTGAACCTGCAAAACAACCGCCTGA  
CTTCCCAGGGCTCCCAGAGAACGGCTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC  
TGACCTTGGCACCCGCTCTGCCAAACCCCTGATCAGTGTGCTGCCAACTATCTCACCAAGATCT  
ATGGGCTCACCTTGGCAGAACGCAAACCTGAGGTCTGTGACTCTGCACAAACAAGCTGGCAGACGCCGGC  
TGCCGGACAAACATGTCACCGCTCAGCAACCTGAGGTCTCATCCTGTCCAGCAACTTCCCTGCCACGTGC  
CCAAGCACCTGCCCTGTCACAGCTCAAGCTGCACCTCAAGAACAAACAGCTGGAGAACAGATCCCCGGGGCCT  
TCAGCGAGCTGAGCAGCTGCGAGCTATACTGCAGAACAAACTACCTGACTGACGAGGGCCTGGAACAGAGA  
CTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCAGCAACAACCTGTCTCGGGTCCCAGCTGGCTGC  
CGCGCAGCCTGGTGTGCTGCACCTGGAGAACAGCCATCCGGAGCGTGGACCGAATGTGCTGACCCCCATCC  
GCAGCCTGGAGTACCTGCTGTCACAGCAACCAGCTGCCGGAGCAGGGCATCCACCCACTGGCCTCCAGGGCC  
TCAAGCGGTTGACACGGTGCACCTGTACAACAAACCGCTGGAGGCCGTGCCAGTGGCCTGCCCTCGCCGCGTGC  
GCACCCCTCATGATCCTGCACAAACAGATCACAGGCAATTGGCCGGAAGACTTGGCACCACCTACTTCTGGAGG  
AGCTAACCTCAGCTACAACCGCATCACCAGCCCACAGGTGACCCGACGCCCTCCGCAAGCTGCCCTGCTGC  
GCTCGCTGGACCTGTCGGCAACCAGCTGCACACGCTGCCACCTGGGCTGCCATGGCTGAAATGTCCATGTGCTGAAGG  
TCAAGCGCAATGAGCTGGTGCCTTGGCACAGAGGGCGCTGGCGGATGGCTCAGCTGCGTGAAGCTGTACCTCA  
CCAGCAACCGACTGCGCAGCCCTGGGCCCCGTGCCCTGGTGGACCTGCCCATCTGCAGCTGCTGGACA  
TCGCCGGAAATCAGCTCACAGAGATCCCCGAGGGCTCCCCGAGTCACCTGAGTACCTGTACCTGCAGAACACA  
AGATTAGTGCCTGGCCCGCAATGCTTCGACTCCACGCCAACCTCAAGGGATCTTCTCAGGTTAACAAAGC  
TGGCTGTGGCTCCGGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAGGTCTTGGACATTGAAGGCAACT  
TAGAGTTGGTGCACATTTCAAGGACCGTGGCCCTGGGAAGGAAAGGAGGAGGAGGAAGAGGAGGAGGAGG  
AGGAAGAGGAAACAAAGATAGTGCACAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGACTCTTTCTGC  
AGCACACGCCCTGTGTGCTGTGAGCCCCCACTCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA  
TCCCACATGACACAGGGCTGACACAGCTCATATCCCCACCCCTTCCACGGCGTGTCCCACGGCCAGACACATGC  
ACACACATCACACCCCTCAAACACCCAGCTCAGCCACACACAACACTACCCCTCCAAACCAACACAGTCTGTACAC  
CCCCACTACCGCTGCCACGCCCTGTAATCATGCAGGGAAAGGGCTGCCCTGCCACACACAGGCACCC  
TTCCCTCCCCCTGCTGACATGTGATGCGTATGCATACACACACACACATGCACAAAGTCATGTGCGAA  
CAGCCCTCCAAAGCCTATGCCACAGACAGCTTGTGCCAGGAAATCAGCCATAGCAGCTGCCGTCTGCC  
GTCCATCTGTCGCTCCGTTCCCTGGAGAACACACAAGGGTATCCATGCTGTGGCCAGGTGCCCTGCCACCCCT  
GGAACCTACAAAAGCTGGTTTATTCTTCCATCTATGGGGACAGGAGCCCTCAGGACTGTGGCTGGCC  
TGGCCCAACCTGCTCCAGGTGCTGGGAGTCAGTCACCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA  
CAGGCACCTTCCAATGGCAAGCCAGTGGAGGAGGAGGCCCTGGGTGCTGTGGGGCTTGGGG  
CAGGAGTGAAGCAGAGGTGATGGGCTGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTT  
GTTCTCAGGCCTGTGGGGAAAGTCCGGTGCCTTATTCTTATTCTTCTAAGGAAAAAAATGATAAAAAT  
CTCAAAGCTGATTTCTTGTATAGAAAACATAATAAAAGCATTATCCCTATCCCTGCAAAAAAA

## FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPPEENEFAEEEPLVLSPEEPGPGPAAVSCP RD CACS QEGVVDCGGIDLREFPGDLP  
EHTNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKA FEHLTNLYLYLANNK  
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHN NKLA DAGLPDNMFNGSSNV  
EV LILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN  
ETFWKLSSLEYLDLSSNNLSRVPA GLPRSLVLLHLEKNAIRSDANVLTPIRSLEYLLLHSN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLP RRVRTLMILHNQITGIGREDFATTYF  
LEELNLSYNRITS PQVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWDLAHLQ LLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANA FDSTPNLK GIFLRFNKLAVGSVVDSA FRRLKHLQVLDIEGNLEFGDISKD  
RGRLGKEKEEEEEEEEEEETR

**Signal sequence:**

amino acids 1-48

**N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

**Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

**N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

**Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

## **FIGURE 109**

## FIGURE 110

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP  
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCDVDECATGRASCPRFRCQ  
VNTFGSYICKCHKGFDLMIIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG  
DGLTCVYIPKVMIEPSGPIHPKGNGTILKGDTGNNNWIPDVGSTWWPPKTPYIIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTPERPTTGLTTIAPAASTPPGGITVDN  
RVQTDPQKPRGDVFSLVHSCNFDHGLCGWIKEKDNDLHWEPIRDAGGQYLTVSAAKAPGG  
KAARLVLPLGLRGMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI  
TLRGADIKSESQR

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 273-277

**Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

**Tyrosine kinase phosphorylation site.**

amino acids 199-206

**N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

**Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

**Cell attachment sequence.**

amino acids 382-385

**EGF-like domain cysteine pattern signature.**

amino acids 75-87

## **FIGURE 111**

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTGCCCTTAGATTGTGA  
AATGTGGCTCAAGGTCTTCACAACTTCCCTTGC~~A~~ACAGGTGCTGCTCGGGCTGA  
AGGTGACAGTGC~~C~~ATCACACACTGTCCATGGCGTCAGAGGT~~C~~AGGCCCTACCTACCCGTC  
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCA  
ACAATGCCAAATACTTACTGGGCTGTGAATAAGTCTGTGGTCTGACTTGAATACC  
AACACAAGTCACCATGATGCCACCCATGCATCTGCTTATCAACCCACTGCAGTCCCT  
GATGAAGGCAATTACATCGTGAAGGTCAACATT~~C~~AGGAAATGGA~~A~~CTCTATCTGCCAGTCA  
GAAGATA~~C~~ACAAGTCACGGTTGATGATCCTGT~~C~~ACAAAGCCAGTGGTG~~C~~AGATT~~C~~ATCCTCCCT  
CTGGGCTGTGGAGTATGTGGGAACATGACCC~~T~~GACATGCCATGTGG~~A~~GGGGCACTCGG  
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGT~~C~~ACACCAGCTCCACCTACTCCTTTC  
TCCCCAAAACAATACCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGAAATTACAGCT  
GCCTGGTGAGGAACCC~~T~~GTCAGTGAATGGAAAGT~~G~~ATATCATTATGCC~~C~~ATCATATATTAT  
GGACCTTATGGACTTCAGTGAATTCTGATAAAAGGGCTAAAGTAGGGGAAGT~~G~~TTACTGT  
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGGC~~T~~CGCTTAGAAGTT  
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGCTTACAACAACATAAC  
CGGCAGGCAAGATGAAACTCATT~~T~~CACAGTTATCATCACTCCGTAGGACTGGAGAAGCTG  
CACAGAAAGAAAATCATTGTCACCTTAGCAAGTATAACTGGAATATCACTATT~~T~~TGATT  
ATATCCATGTGCTTCTCTTCTATGGAAAAAATATCAACCC~~T~~ACAAAGTTATAAAACAGAA  
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG  
CTCTGGATGACTCGGAATATATGAATTGTTGCTTCCAGATGTTCTGGT~~G~~TTCCAGG  
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTG~~T~~TGTATGGGCAAGATTGCACAGTACAGT  
GTATGAAGTTATT~~C~~AGCACATCC~~T~~GCCAGCAGCAAGACC~~T~~CCAGAGTGAACTT~~C~~ATGG  
GCTAAACAGTACATT~~C~~GAGTGAAGAAATTCTGAAGAAACATT~~T~~AAGGAAAACAGTGGAAAAGT  
ATATTAA~~T~~CTGGAATCAGTGAAGAAACCAGGACCAACACCTCTACTCATTATT~~C~~TTACA  
TGCAGAA~~T~~AGAGGCATTATGCAAATTGA~~A~~CTGCAGGTTT~~C~~AGCATATA~~C~~ACAATGT~~C~~TT  
GTGCAACAGAAAACATGTTGGGAAATATT~~C~~CTCAGTGGAGAGTCGTTCTCATGCTGACGG  
GGAGAACGAAAGTGACAGGGTT~~C~~CATAAGTTGTATGAA~~A~~ATCTACAAACCTCA  
ATTAGTTCTACTCTACACTTC~~A~~CTATCATCAACACTGAGACTATCCTG~~T~~TCACCTACAAA  
TGTGGAAACTTTACATTGTTG~~C~~ATT~~T~~T~~C~~AGCAGACTTTGTTTATTAAATT~~T~~TATTAGTG  
TTAAGAATGCTAAATT~~T~~TATGTTCAATT~~T~~TATT~~C~~AAATT~~T~~TCTATCTTGTATTGTACAA  
CAAAGTAATAAGGATGGTTGT~~C~~ACAAAAAA~~A~~CTATGCCTCTCTTTTTCAATCACC  
AGTAGTATT~~T~~TGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGT~~C~~TTATT~~T~~T  
TTTTTTCAAGGAAAGATGGATTCAAATAATTATTCTGTTTGT~~T~~TTAAAAA~~A~~AAAAA

## FIGURE 112

MWLKVTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQI IWLFERPH  
TMPKYLLGSVNKSVPDLEYQHKFTMMPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ  
KIQVTVDPPVTKPVVQIHPPSGAVEYVGNMTLTCHEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV  
DLGEAILFDCSADSHPPNTYSWIRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT  
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSVPASDCVSGQDLHSTV  
YEVIQHIPAQQQDHPE

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 341-359

**N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

**Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

**Tyrosine kinase phosphorylation site.**

amino acids 272-280

**N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 113**

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTGCAGTTCCCCTGGCAGTCCTGGTGTGTT  
GCTTGGGGTGCTCCCTGGACGCACGGCGGGAGCAACGTTCGCGTCATCACGGACGAGA  
ACTGGAGAGAAACTGCTGGAAAGGAGACTGGATGATAGAATTTATGCCCGTGGTGCCTGCT  
TGTCAAAATCTCAACCGGATGGAAAGTTGCTGAATGGGAGAAGATCTTGAGGTTAA  
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC  
TTCCTACTATTATCATTGTAAGATGGTGAATTAGGCCTATCAGGGTCCAAGGACTAAG  
AAGGACTTCATAAAACTTATAAGTGATAAAGAGTGGAAAGAGTATTGAGCCGTTCATCATG  
GTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA  
TCAGGACGTGCCATAACTACTTTATTGAAGACCTGGATTGCCAGTGTGGGATCATATACT  
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC  
AGATTGCCTTGTCCCTCAAAAAGGCCAGACCCACAGCCATACCCATACCCCTCAAAAAAAT  
TATTATCAGAACTGCACAACCTTGAAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA  
GATGTTCAGAAGAAGAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC  
CATAAAGACAACGCTCTGGGTCCATCATTGCCACAGATAAATCCTAGTTAAATTTATAG  
TTATCTTAATATTATGATTTGATAAAACAGAACAGATTGATCATTGTTGGTTGAAGTG  
AACTGTGACTTTTGAAATTGCAAGGTTCAGTCTAGATTGTCATTAAATTGAAGAGTCTA  
CATTCAGAACATAAAAGCACTAGGTATACAAGTTGAAATATGATTTAAGCACAGTATGATG  
GTTAAATAGTTCTAATTTGAAAAATCGTGCCAAGCAATAAGATTATGATATTGT  
TTAATAATAACCTATTCAAGTCTGAGTTTGAAAATTACATTCCCAAGTATTGCATTAT  
TGAGGTATTTAAGAAGATTTTAGAGAAAATTCTCATTTGATATAATTTCTCTG  
TTCACTGTGAAAAAAAGAAGATTTCCATAAATGGGAAGTTGCCATTGTCTCAAG  
AAATGTGTTCACTGACATTCGGGTTTTTAGAGGTATTCAGTTCTACACA  
ATTTTTAGGTATGCAACTAAAAAACTACCTTACATTAATTACAGTTCTACACA  
TGGTAATACAGGATATGCTACTGATTAGGAAGTTTAAGTTCATGGTATTCTCTTGATTC  
CAACAAAGTTGATTCTCTGTATTTTCTTACTACTATGGTTACTTTTTATTTT  
CAAATTGGATGATAATTCTGGAAACATTTTTATGTTAGAAACAGTTTTTTTGTT  
GTTCAAACGTGAAGTTACTGAGAGATCCATCAAATTGAACAACTGTTGTAATTAAAAATT  
TTGGCCACTTTTCAGATTTCATCATTCTGCTGAACTTCAACTGAAATTGTTTTT  
TTCTTTGGATGTAAGGTGAACTTCCCTGATTTTGCTGATGTGAAAAGCCTGGT  
TTTACATTTTGAAATTCAAAGAAGCTTAATATAAAAGTTGCATTCTACTCAGGAAAAAAG  
CACTTCTTGTAATGCTTAAATGTATTTTGCCTCATATACAGAAAGTTCTTAATTGAT  
TTTACAGTCTGTAATGCTGATTTTAAATAAACATTTTTATTTTTAAAGACAA  
ACTTCATATTATCCCTGTTCTTGACTGGTAATATTGTGGGATTTCAGGTAAAA  
GTCAGTAGGATGGAAACATTTAGTGATTTTTACTCTTAAAGAGCTAGAATACATAGTTT  
CACTTAAAGAAGGGGAAATCAAAATACAATGAATCAACTGACCCATTACGTAGTAGAC  
AATTCTGTAATGCCCTTCTTCTAGGCTGTGCTGTGTAATCCATTAGATTTACAG  
TATCGTAATACAAGTTCTTAAAGCCCTTCCTTTAGAAATTAAATATTGACCATT  
AAAGAGTTGGATGTACTGTATTGATGCCTTAGAAAAAATCTAAGCACAAATAAACTT  
CTTAACCACTTCATTAAAGCTGAAAAAAAAAA

## FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE  
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 182-201

**Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

**Tyrosine kinase phosphorylation site.**

amino acids 107-115

**N-myristoylation site.**

amino acids 20-26, 192-198

**Amidation site.**

amino acids 25-29

## **FIGURE 115**

GCGAGTGTCCAGCTCGGGAGACCCGTGATAATTGTTAACTAATTCAACAAACGGGACCCTT  
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGACAGGGGATTGGAAGAGCGGG  
AAGGTCTGGCCCAGAGCAGTGTGACACTTCCTCTGTGACCTGAAACTCTGGGTGTCTGC  
ATTGCTGATGGCTGGTTGGTGTCTGAGCTGTGCAGGCCAATTCTCACCTCTATTG  
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC  
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGCCAACAAAATGGAAGCCTTGAC  
TAGCAAGTCAGCTGCTGATGCTGAGGGTACCTGGCTCACCTGTGAATGCCTACAAACTGG  
TGAAGCGGCTAACACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA  
GGTTTATGCCAACCTCTGTGCAGCGGCAGTTCTCCCCACTGATGAGGACGAGATAGG  
AGCTGCCAACAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA  
GAGGGAACTTCAGGAACCAAGTACAGGCAATGCTGAGTGTGGATGACTGCTTGGATG  
GGCGCTCGGCCTACAATGAAGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT  
AAAGCAGCTGATGCCGGGGAGGAGGCCACCAACCAAGTCACAGGTGCTGGACTACCTCA  
GCTATGCTGCTTCCAGTTGGGTGATCTGCACCCTGGAGCTCACCGCCGCTGCTC  
TCCCTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGGTACTTGTAGCAGTTATTGGA  
GGAAGAGAGAAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAGGCA  
TCTATGAGAGGCCTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTGTGCTGG  
GAGGGTGTCAAACGTACGCTCATGGCTTCTGAGACAGAAGAGGCTTCTGTAGGTACCA  
CAGGGCCCCACAGCTGCTCATTGCCCTCAAAGAGGAGGACGAGTGGACAGCCGCACA  
TCGTCAGGTACTACGATGTCATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA  
CCTAAACTTGACGAGCCACCGTTGATCCAAGACAGGAGTCTCACTGTCGCCAGCTA  
CCGGGTTTCAAAGCTCCTGGCTAGAGGAAGATGATGACCTGTTGTGGCCGAGTAAATC  
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT  
TATGGAGTGGGAGGACAGTATGAACCGCACTCGACTTCTCTAGGCAGCTTGTACAGCGG  
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG  
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGT  
TTCTGGTACAACCTCTTGCAGGGAGGAGGAAAGGTGACTACCGAACAGACATGCTGCTGCC  
TGTGCTTGTGGCTGCAAGTGGTCTCCAATAAGGTTCCATGAACGAGGACAGGAGTTCT  
TGAGACCTTGTGGATCAACAGAAGTTGACTTGACCATCCTTCTGTCTCCCTCCTGGTC  
CTTCAGCCCATGTCACAGTGCACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT  
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT  
GTGACTGAAGTCCCAGCCCTTCATTAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA  
AAGTGGCTGAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCCTTGTACCTCAGGTGTT  
TTAGGTGTGAGATGTTCACTGAAACCAAGTTCTGATACCTGTTACATGTTGTTTAT  
GGCATTCTATCTATTGTGGCTTACCAAAAAAATGTCCCTACCAGAAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP  
TDEDEIGAAKALMRLQDTYRLDPGTISRGEELPGTKYQAMLSVDDCFGMGRSAYNEGYYHTV  
LWMEQVLKQLDAGEEATTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR  
YFEQLLEEREKTLTNQTEAELATPEGIYERPVDFYLPERDVYESLCRGEVKLTPRRQKRLF  
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYVDVMSDEEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS  
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPLGAAIWPKGTAVFWYNLLRSGEDYR  
TRHAACPVLVGCKWSNKWFHERGQEFLRPCGSTEVD

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 115-119, 264-268

**Glycosaminoglycan attachment site.**

amino acids 490-494

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

**Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

**N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

**Leucine zipper pattern.**

amino acids 213-235

## **FIGURE 117**

GCAGTATTGAGTTTACTCCTCCTTTAGTGGAAAGACAGACATAATCCCAGTGTGAGTGAAATTGATTGT  
TTCATTTATTACCGTTGGCTGGGGTTAGTTCCGACACCTTCACAGTTGAAGAGCAGGCCAGAAGGAGTTGTA  
AGACAGGACAATCTTCTTGGGGATGCTGGTCTGGAAAGCCAGCAGGGCCTTGCCTGTCTTGGCCTCATGACCC  
CAGGTCTCTGGTAAACACTGAAAGCCTACTACTGGCCTGGTCCCCATCAATCCATTGATCCTTGAGGCTGTGCC  
CCTGGGCACCCACCTGGCAGGGCTACCACCATGCGACTGAGCTCCCTGTTGGCTCTGCTGCCAGCGCTTC  
CCCTCATCTTAGGGCTGCTCTGGGGTGCAGCCTGAGCCTCTGCGGGTTCTGGATCCAGGGGAGGGAGAAG  
ATCCCTGTGTGGAGGCTGTAGGGGAGCGAGGAGGCCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG  
ATGAAGACTTCAAACCCCGATTGCCCCACTACAGGGACCCACAAGCCTACAAGAAGGTGTCAGGACTC  
GGTACATCCAGACAGAGCTGGGCTCCCGTGAGCGGTTGCTGGTGGCTGCACCTCCCAGCTACACTGTC  
CTTTGGCGTGGCTGTGAACCGTACGGTGGCCCACCTCCCTCGGTTACTCTACTTCACTGGGAGCGGGGG  
CCCGGGCTCCAGCAGGGATGCGAGGGTGTCTCATGGGATGAGCGGCCGCTGGCTCATGTCAGAGACCCCTGC  
GCCACCTTACACACACTTGGGGCCGACTACGACTGGTCTTCATCATGCAAGGATGACACATATGTGCAGGCC  
CCCGCTGGCAGCCCTGCTGGCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGCAGAGGAGTTCAATTG  
GCGCAGGCAGCAGGGGGTACTGTCTAGTGCATGGGGCTTGGCTACCTGTTGTCACGGAGTCTCCTGCTTC  
GGCCACATCTGGATGGCTGCCAGGGAGACATTCTCAGTCCCCTGCTGACGAGTGGCTTGGACGCTGCCCTCATTTG  
ACTCTCTGGCGTGGCTGTCTCACAGCACCAGGGCAGCAGTATGCTCATTTGAACCTGGCCAAAATAGGG  
ACCTGAGAAGGAAGGGAGCTGGCTTCTGAGTGCCTTCCGGTGCACCTGTCATCCGAAGGTACCCCTCATGT  
ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGCTTACAGTGAATAGAACAACTGCAAGGCTCAGA  
TCCGGAACCTGACCGTGTGACCCCCGAAGGGGAGGCAAGGGCTGAGCTGGCCGTTGGCTCCCTGCTCCTTCA  
CACACACACTCGCTTGGAGGTGCTGGCTGGACTACTTCACAGAGCAGCACACCTCTCCTGTCAGATGGG  
CTCCAAGTGCCACTACAGGGGGTAGCAGGGCGACGGTGGTGTAGCGTGGAGACTGCCCTGGAGCAGCTCA  
ATCGCGCTATCAGCCCCGCTGCCTCCAGAAGCAGCGACTGCTCAACGGTATCGCGCTTCGACCCAGCAC  
GGGCATGGAGTACACCCCTGGACCTGCTTGGAAATGTTGACACAGCGTGGCACCGGGGGCCCTGGCTCGCA  
GGTCAGCCTGCTGCCACTGAGCCGGTGGAAATCCTACCTATGCCCTATGTCACTGAGGCCACCGAGTGC  
AGCTGGTGTGCCACTCTGGTGGCTGAAGCTGCTGCAGCCCCGGTTCTCGAGGGCTTGCAGCCAATGTCC  
TGGAGCCACGAGAACATGCTTGTGCTACCCCTGTTGCTGGTCTACGGGCCACGAGAACGGTGGCCGGAGCTCCAG  
ACCCATTCTGGGTGAAGGCTGCAGCAGGGAGTTAGAGCGACGGTACCCCTGGACGAGGCTGGCTGGCTCG  
CTGTGCGAGCAGAGGCCCTTCCCAGGTGCGACTCATGGACGTGGTCTGAAGAACAGCACCCTGTGGACACTCTCT  
TCTTCTTACCAACCGTGTGGACAAGGCCCTGGCCGAAGTCTCAACGCTGTGCGATGAATGCCATCTGCT  
GGCAGGCCCTTCTCAGTCCATTCCAGGAGTTCAATCCCTGCCCTGTCAACCACAGAGATCACCCCCAGGGCCCC  
CGGGGGCTGGCCCTGACCCCCCTCCCTGGTGTGCTACCCCTCCGGGGCTCCTATAGGGGGAGATTG  
ACCGGCAGGCTTGTGGAGGGCTGCTTACACGCTGACTACCTGGCGGCCGAGCCGGCTGGCAGGTGAAC  
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGGGCTGGAGGGTGTGGATGTTCTCGGCTTCAGGGCTCC  
ACCTCTTCGGCCGTAGAGCCAGGGCTGGTGCAGAACGTTCTCCCTGCCAGACTGAGGCCACGGCTCAGTGAAG  
AACTCTACCAACCGCTGCCCTCAGAACCTGGAGGGCTAGGGGCCGTGCCAGCTGGCTATGGCTCTTGT  
AGCAGGAGCAGGCCATAGCACTTAGCCCGCTGGGGCCCTAACCTCATACCTTGTCTGCCAGCC  
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTAAATATGAAAATGTTATTAA  
ACATGCTTCTGCC

## **FIGURE 118**

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD  
QSDEDFKPRIVPYYRDPNPKVVKLTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV  
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHFGADYDWFFIMQDDTY  
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLRLRPHLDGCRG  
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPGEAGLSWPVGLPAPFTPNSRFEV  
LGWDYFTEQHTFSCADGAPKCPHQASRADVGDALETALEQLNRRYQPRLRFQKQRLLNGYR  
RFDPARGMEYTL DLL ECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLPPLL  
VAEAAAAPAFLEAFAAVNLEPREHALLTLLL VYGPREGGRGAPDPFLGVKA AAAE LERRYPG  
TRLAWLAVRAEAPSQVRLMDVSKKHPVDTLFFLTTVWTRPGPEVLRCRMNAISGWQAFFP  
VHFQEFPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA  
RARLAGELAGQEEEALEGLEVMDFVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR  
CRLSNLEGLGGRAQLAMALFEQEQANST

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 489-507

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## **FIGURE 119**

CGGAGTGGTGCACGTGAGAGGAAACCGTGCACGGCTGCCTTCCTGTCCCCAAGCC  
GTTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTTGG  
AACCATTTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGCATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTCA  
GAGGATGAGCGATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTTGTAAAACC  
CAAAGATGTGAGTCTTGGGCTGCAGTAAAGGAGACTGGACAAACACTGTGACAAAGCAG  
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCAATTAAATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACAAC  
GTTCTCCTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA  
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT  
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTAACAGCCTCT  
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAAGAAATGCAGAAGATGCTGATGGA  
AAAGATGTATTAATACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC  
CAACCAGGTAGTAGAAGGCTTGTTCAGATATGGCTTACTTTAATGGACTGACTCCAA  
ATCAGATGCATGTGATGTATGGGTATACCGCCTAGGGCATTGGCATTTCAAT  
GATGCATTGGTTTCTTACCTCAAATGGTCTGACAATGACTGAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTGTATAGGACGTGTGTCATTATTGTAGTAGTAACATATCCAA  
TACAGCTGTATGTTCTTTCTTTCTAATTGGTGGCACTGGTATAACCACACATTAAAG  
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAAACACATGAACATTGAAATG  
TGTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAATAAACTATTAATAAAATTATAT  
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTGCTGATTGGTT  
AAAAAAATTAAACAGGTCTTAGCGTTCAAGATATGCAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAAGTAAAACCTTGTGTTCCCTTACTTCTAATACGTATTGATTGTTCT  
AAGCCTCCCCAAGTTCCAATGGATTGCTTCTCAAAATGTACAACTAAGCAACTAAAGAAA  
ATTAAAGTGAAAGTTGAAAAT

## FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME  
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAFFSSENVKFESINMDTNMDWLMMRK  
AYKYAFDKYRDQYNWFFLARPTTFAIENLYFLLKKDPSQPFYLGHТИKSGDLEYVGMEGG  
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHI FNDALVFL  
PPNGSDND

**Signal sequence:**

amino acids 1-33

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## FIGURE 121

## FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELSCNYGSGSVKNCCPLNWEYFQSSCYFFSTDТИSWALSLKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLEDCATMRDSS  
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

**Signal sequence:**

amino acids 1-42

**N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

**Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

**N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

## FIGURE 123

GGGACTACAAGCCGCGCCGCTGCCGCTGGCCCCCTCAGCAACCCCTGACATGGCGCTGAGGCAGGCCACCGCGAC  
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCCGTGCTGCTGCTTTCAAGGGCTGCCTGATAGGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCCAGTGGTACAGGAATTGAAAGTGTGGAACTGTCTTGATCATTACGGATTGCG  
AGACAAGTGACCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACAACAAAA  
TTCAGGGAGACTTGGCGGGCTGAGAAATACTGGGAAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCTTATCGCTGTGAGGCTGCTGCAAATGACCGAAGGAATTGATGAGATTGTGATCGAGTAA  
CTGTGCAAGTGAAGCCAGTGCACCCCTGTCTGTAGAGTGGCAAGGCTGTACCAAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGAGGGCCACCCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT  
CCAGAGCCAATCCCAGATTGCAATTCTTCCACTTAAACTCTGAAACAGGCACTTGGTGTCACTGCTG  
TTCACAAGGACGACTCTGGGCAGTACTACTGCAATTGCTTCAATGACGCAGGCTCAGCCAGGTGTAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGTCTGGTGTCTGCTGTACTGGCCCTGA  
TCACGTTGGGCATCTGCTGTGATCACAGACGGCTACTTCATCAACAATAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGAAACAGATGGAGTTAACTACATCCGCACTGACGAGGGCCACTTCAGACACAAGTCATCGTTG  
TGATCT**G**A GACCCCGGGTGTGGCTGAGAGCGCACAGAGCGCAGTGCACATACCTCTGCTAGAAAACCTCTGCTAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGCAGACTCATTCAGAAGCTTCTGTTGGCAAAGTTGACCA  
CTACTCTTCTTACTCTAACAGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAAATAACCAAA  
GGAAGCGAAACTGGGTGCGTCACTGAGTTGGTCTTAATCTGTTCTGGCTGATTCCCGATGAGTATTAGG  
GTGATCTTAAAGAGTTGCTCACGTAACGCCCCTGCTGGCCCTGTGAAGCAGCATGTTACCACTGGTCGTT  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCGGGGAAACCA  
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATGGCCACAGACACCACCGCAGTTCTTAAAGGCTCTG  
TGATGGTGTGAGTGTCCATTGAGGAGAGCTTTGGATCAGCATTTGTTAAACAAACCAAAATCAGGAAG  
GTAAATTGGTTGCTGAAAGGGATCTGCTGAGGAACCTGCTGTCCAACAGGGTGTCAAGGATTTAAGGAAA  
ACCTCGTCTTAGGCTAACGTCTGAAATGGTACTGAAATATGTTTCTATGGGTCTGTTATTAAACCAAA  
TACATCTAAATTGGTCAAGGATGTATTGATTATTGAAAAGAAAATTCTATTAAACTGTAATATATTGT  
CATACAATGTTAAATAACCTATTGGTAAAGGTTCAACTTAAGGTTAGAAGTCTCAAGCTACTAGTGTAAAT  
TGGAAAATATCAATAATTAGTATTGTTACCAAGGAATCCTCATGGAAGTTACTGTGATGTTCTTTCT  
CACACAAGTTTAGCCTTTTCAACAGGAAACTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAATTCAGTTAACGCAATGTTGAAATCAGTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTGA  
GCCTCTCCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAACGCCTCAGATGTACATACAGATG  
CCAGTCAGCTCTGGGGTGCAGGCCAGGGCCGGCGCTAGCTCACTGTCCTGCTGCTGCCAGGAGGCC  
GCCATCCTGGCCCTGGCAGTGGCTGTGCTCCAGTGAGCTTACTCACGTGCCCTGCTCATCCAGCACAGC  
TCTCAGGTGGGACTGCAGGGACACTGGTGTCTCCATGCTAGCGTCCCAGCTTGGCTCTGTAACAGACCT  
TTTGTTATGGATGGCTCAAAAATAGGGCCCAATGCTATTGTTAAAGTTGTTAATTATTGTT  
AAGATTGCTAAGGCCAAGGCAATTGCAAAATCAAGTCTGCAAGTACAATAACATTAAAAGAAAATGGAT  
CCCACGTGTTCTTGCACAGAGAAAGCACCCAGGCCACAGGCTCTGCTGCAATTCAAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCTGGGGAGGAAAG  
TGAAAAGCCTGAATCAAAGCAGTTCTAATTGACTTTCAATTTCATCCGCCGAGACACTGCTCCATT  
TGTGGGGGACATTGCAACATCACTCAGAAGCCTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCC  
GCCGTGCTGGACTCAGGACTGAAGTGTGAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGCTGG  
GAATGGCTCTCAACTCACCTGCTTTCAGCTTCAAGTGTCTGGTTTATACTTGCAGCTTTTT  
AATTGCATACATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGCCGCAGGCCGCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTGCTGCATGGCATCTGGATGCTAGCATGCAAGTTC  
CCTCCATCATTGCCACCTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCCTGGGATTACGCTCCAGCCTC  
TCTTGGTTGTCAAGTGTAGGGTAGCCTTATTGCCCCCTTCTTACCCCTAAACCTTCTACACTAGTGC  
TGGGAACCAGGTCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGTATTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT  
GCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC  
CTCATTATAAAAGCTTCAAAAAACCCA